

PR 17-SEP-2001; 2001FR-0011978.
XX (MOLE-) MOLECULAR ENGINES LAB.
PA Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-313353/30.
XX New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
XX
XX Disclosure; Page 447; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15
XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
XX sequence that hybridizes to them under highly stringent conditions, or
XX the complement of any of them, or the corresponding RNA. The novel
XX isolated nucleic acids of the invention are useful as probes and primers
XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
XX and for production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention.
XX
XX Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
XX
XX Query Match 1.2%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1616 TAAATATATAATTGTT 1631
XX |||||
XX 17 TAAATATATAATTGAT 2
XX
XX RESULT 136
XX AAT32141
XX ID AAT32141 standard; DNA; 18 BP.
XX AC AAT32141;
XX DT 16-SEP-1996 (first entry)
XX DE DNA sequencing "primer" (primer/linker) complementary sense strand.
XX KW Sense strand; DNA sequencing; oligonucleotide; primer;
XX KW primer; linker; priming site; labelling region; cohesive end;
XX KW complementary strand; ds.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..18
XX /*tag= a
XX /note= "forms doubled stranded segment when
XX bound to nucleotides 5-22 of the
XX sequence given in AAT12342"
XX
XX WO9602673-A1.

PD 01-FEB-1996.
XX
XX 14-JUL-1995; 95WO-US08894.
XX
XX 14-JUL-1994; 94US-0275169.
XX 25-FEB-1994; 94US-0202400.
XX
XX (AMIC-) AMICON INC.
XX (GRAC) GRACE & CO-CONN W R.
XX Leonard JT;
XX
XX WPI; 1996-105934/11.
XX
XX New oligo:nucleotide(s) for DNA sequencing - having a priming site,
XX a labelling region and a cohesive end complementary to a restriction
XX fragment sequence
XX
XX Disclosure; Page 5; 23pp; English.
XX
XX The present sequence is an example of a complementary sense strand
XX from a novel DNA sequencing oligonucleotide called a "primer"
XX (primer/linker), which comprises a priming site, labelling region,
XX cohesive end and complementary strand. The priming site is the
XX optimal target for annealing prior to treatment with polymerase.
XX The labelling region is a template sequence which directs DNA
XX polymerase to incorporate multiple labelled, e.g. radioactive
XX nucleotides. The cohesive end provides compatible ends
XX for ligation of primers to restriction fragments. The
XX complementary strand provides a region of double stranded DNA which
XX is required by DNA ligases for the attachment of the primer to a
XX restriction fragment.
XX A prefd. sequencing procedure comprises the generation of
XX restriction fragments from the DNA mol. to be sequenced, ligation
XX of primers to the fragments, sepn. and purificn. of primer
XX attached restriction fragments, conc. and buffer exchange,
XX generation and sepn. of sequencing prods., exposure of X-ray film
XX to sequencing prods. and detection of the signal on the film.
XX
XX Sequence 18 BP; 14 A; 2 C; 1 G; 1 T; 0 other;
XX
XX Query Match 1.2%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 516 ACAAAAACACAAAT 631
XX |||||
XX 2 ACAAAAACACAAAT 17
XX
XX RESULT 137
XX ABZ10520/c
XX ID ABZ10520 standard; DNA; 18 BP.
XX AC ABZ10520;
XX XX
XX DT 16-JAN-2003 (first entry)
XX DE Haematopoietic cell proliferation disorder related oligonucleotide #660.
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
XX KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX KW cytosine methylation state; probe; primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX WO200277272-A2.
XX 03-OCT-2002.
XX 26-MAR-2002; 2002WO-EP03401.

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PR 26-MAR-2001; 2001US-278333P.
XX (EPIC-) EPICENOMICS AG.
PA Berlin K, Braun A, Distler J, Gueig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
PI Pellet C, Schwöpe I, Ziebarth H;
XX WPI; 2003-018942/01.
DR Detecting and differentiating between hematopoietic cell proliferative
XX disorders, comprises contacting a target nucleic acid with a reagent
PT that distinguishes between methylated and non-methylated CpG
PT dinucleotides -
XX
XX Claim 15; Page 48; 117pp; English.
XX The present invention describes a method for detecting and
XX differentiating between haematopoietic cell proliferative disorders
XX associated with at least 1 gene and/or their regulatory regions in a
XX subject. The method comprises contacting a target nucleic acid in a
XX biological sample obtained from the subject with at least 1 reagent,
XX which distinguishes between methylated and non-methylated CpG
XX dinucleotides within the target nucleic acid. AB209861 to AB211118
XX represent specifically claimed nucleotide sequences from the present
XX invention. Oligonucleotides from the present invention can be used for
XX differentiating between healthy haematopoietic cells and proliferative
XX disorder haematopoietic cells; for differentiating between acute
XX lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
XX determining the cytosine methylation state and/or single nucleotide
XX polymorphisms (SNPs) of haematopoietic cell proliferation disorder
XX related sequences and their complements; and as primers for the
XX amplification of haematopoietic cell proliferation disorder related
XX DNA sequences. The nucleotide sequences from the present invention can
XX also be used for detecting a predisposition to, differentiation between
XX subclasses, diagnosis, prognosis, treatment and/or monitoring of
XX haematopoietic cell proliferative disorders. The present method enables
XX a highly specific classification of haematopoietic cell proliferative
XX disorders allowing for improved and informed treatment of patients.
XX
XX Sequence 18 BP; 4 A; 0 C; 4 G; 10 T; 0 other;
XX
XX Query Match 1.2%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 620 AATACACAAATATT 635
XX ||||| ||||| |||||
XX 17 AATACACAAATATT 2
XX
XX RESULT 138
XX AAQ89232
XX ID AAQ89232 standard; CDNA; 20 BP.
XX AC AAQ89232;
XX XX
XX XX 25-MAR-2003 (updated)
XX DT 20-OCT-1995 (first entry)
XX XX
XX XX Rat opioid receptor PCR primer.
XX DE
XX XX Opioid receptor; gene therapy; diagnostic; primer; PCR;
XX KW polymerase chain reaction; ss.
XX XX Synthetic.
XX OS
XX XX WO9507983-A1.
XX XX
XX XX 23-MAR-1995.
XX PD
XX XX 13-SEP-1994; 94WO-US10358.
XX PF

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XX 13-SEP-1993; 93US-0120601.
XX (INDV) UNIV INDIANA FOUND.
XX Yu L;
XX WPI; 1995-131351/17.
XX New nucleic acid encoding new human mu opioid receptor - and
XX related vectors, transformed cells, antibodies etc., useful in
XX diagnosis, treatment and drug screening.
XX Example 9; Page 154; 266pp; English.
XX PCR using the degenerate primers given in AAQ89231-32 was used to
XX demonstrate that the relative mRNA abundance of mu, delta and
XX kappa opioid receptors, and of a new opioid family member
XX (AAQ89233) in rat brain, was 68, 14, 10 and 8%, respectively.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 20 BP; 5 A; 2 C; 4 G; 7 T; 2 other;
XX
XX Query Match 1.2%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 75.0%; Pred. No. 2.4e+02;
XX Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1121 GTTATAAGATGTTATAGTA 1140
XX ||||| ||||| |||||
XX 1 GCTTACATGTTGTTAGTA 20
XX
XX RESULT 139
XX AAH56684
XX ID AAH56684 standard; DNA; 20 BP.
XX AC AAH56684;
XX XX
XX XX 06-SEP-2001 (first entry)
XX DT
XX XX Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:332.
XX DE
XX XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
XX KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
XX KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
XX KW antibacterial; antiviral; antiproliferative; antisense therapy;
XX KW microbial infection; ss.
XX OS
XX XX Streptococcus pyogenes.
XX XX
XX XX WO200136625-A2.
XX PN
XX XX 25-MAY-2001.
XX PD
XX XX 20-NOV-2000; 2000WO-CA01347.
XX PF
XX XX 18-NOV-1999; 99US-0166249.
XX PR
XX XX (GENE-) GENESENSE TECHNOLOGIES INC.
XX PA
XX XX Wright JA, Young AH, Dugourd D;
XX PI WPI; 2001-355633/37.
XX XX
XX XX Novel antisense compounds targeting nucleic acid encoding groEL or
XX KW groES gene of microorganism, which hybridize with and inhibit
XX PT expression of the genes, useful to inhibit growth of microorganism
XX PT having the genes -
XX PT
XX Claim 3; Page 50; 110pp; English.
XX
XX The present invention specifically claims AAH56368 to AAH56832 which are
XX antisense oligonucleotides to nucleotide sequences encoding groE. More

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CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL
 CC or GS gene and administering (I) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention.
 XX
 SQ Sequence 20 BP; 15 A; 4 C; 1 G; 0 U; 0 other;

Query Match 1.2%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 AAAAACAACAAATTA 633
 DB 4 AAAAACAACAAAGAA 19
 |||||

RESULT 140
 AAF83325
 ID AAF83325 standard; DNA; 20 BP.
 AC AAF83325;

DT 09-JUL-2001 (first entry)

XX Human SAPL cDNA specific primer 4dest4 6f.

XX SAPL; SIT4; SIT4 associated proteins like; human; antidiabetic;
 KW sporulation-induced transcript 4; SAPLA; SAPLB; gene therapy; IDDM;
 KW insulin-dependent diabetes mellitus; PCR primer; ss.

XX Homo sapiens.

OS WO200129213-A1.

PN 26-APR-2001.

XX 19-OCT-2000; 2000WO-GB04027.

XX 19-OCT-1999; 99US-0160400.

XX (WELL) WELLCOME TRUST LTD.

PA (MERI) MERCK & CO INC.

XX Todd JA, Twells RCJ, Hess JW, Hey P, Hey P, Caskey CT, Hammond H;

PI Metzker MJ;

XX WPI; 2001-300338/31.

XX Isoforms of novel gene arising from alternative splicing and encoding
 PT highly related proteins termed as SAPLA and SAPLB, from the IDDM4 locus
 PT on human chromosome 11q13, useful for treating IDDM and other diseases

PS Claim 14; Page 98; 129pp; English.
 XX The invention relates to SAPL [SIT4-(sporulation-induced transcript4)
 CC associated proteins-like] polypeptide, selected from SAPLA polypeptide
 CC isoforms and SAPLB polypeptide isoforms. The SAPL polynucleotides are
 CC useful in gene therapy for treating and preventing insulin-dependent
 CC diabetes mellitus (IDDM). Fragments of the SAPL DNA are useful as primers
 CC and probes. The SAPL polypeptides are useful in screening for a substance
 CC e.g., a peptide or chemical compound, which interacts and/or binds with
 CC them. Sequences AAF83318-350 represent PCR primers specific for the SAPL
 CC cDNA.

SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

Query Match 1.2%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1097 AGAAGATGAATCATTTG 1112
 DB 4 AGAAGATGAATCATTTG 19
 |||||

RESULT 141
 AAA62676
 ID AAA62676 standard; DNA; 19 BP.
 AC AAA62676;

DT 08-JAN-2001 (first entry)

XX Cry2A family gene shuffling PCR primer 1 for.

XX Cry2Aa; Cry2Ab; Cry2Ac; family gene shuffling; recombinant;
 KW nucleic acid diversity; mutagen synthesis; PCR primer; ss.

XX Unidentified.

XX WO200042561-A2.

XX 20-JUL-2000.

XX 18-JAN-2000; 2000WO-US01203.

XX 19-JAN-1999; 99US-0116447.

XX 05-FEB-1999; 99US-0118813.

XX 24-JUN-1999; 99US-0141049.

XX 28-SEP-1999; 99US-0408392.

XX 28-SEP-1999; 99US-0408393.

XX 12-OCT-1999; 99US-0416375.

XX 12-OCT-1999; 99US-0416377.

XX (MAXY-) MAXYGEN INC.

XX Cramerzi A, Stemmer WPC, Minshull J, Bass SH, Welch M, Ness JB;

XX Gustafsson C, Patten PA;

XX WPI; 2000-482862/42.

XX Example; Page 54; 74pp; English.

XX The present sequence is a PCR primer used in a method for shuffling genes
 CC cry2Aa, cry2Ab and cry2Ac. Gene shuffling is a process for
 CC generating recombinant nucleic acids. Oligonucleotide assisted
 CC approaches can be used to produce family shuffled nucleic acids without
 CC isolating or cloning full-length homologous nucleic acids. Family gene
 CC shuffling oligonucleotides are provided by aligning homologous nucleic

CC acid sequences to select conserved regions of sequence identity and
 CC regions of sequence diversity. A plurality of oligonucleotides are
 CC synthesised which correspond to at least one region of sequence
 CC diversity. In this example, the oligonucleotides were spiked into
 CC the assembling mix and PCR was then performed using the present primer.
 CC The method can be used to produce a family of shuffled nucleic acids, to
 CC produce recombinant molecules with greater molecular diversity and to
 CC generate classical mutagens. Homologous nucleic acids with low sequence
 CC similarity and non-homologous nucleic acids are also easily recombined.
 XX
 SQ Sequence 19 BP; 9 A; 0 C; 3 G; 7 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1102 ATGAATCATGTTGATGAAA 1120
 ||||| ||||| ||||| |||||
 DB 1 ATGAATCATGTTGATGAAA 19

RESULT 142
 AAA83135
 ID AAA83135 standard; DNA; 19 BP.
 AC AAA83135;
 XX
 DT 04-DEC-2000 (first entry)
 DE cdk7 ribozyme binding site #56.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 PS WPI; 2000-412314/35.

XX
 CC New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 CC RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 CC PCNA and Cyclin B1 -
 XX
 PS Disclosure; Page 57; 109pp; English.
 XX

XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 SQ Sequence 19 BP; 9 A; 0 C; 3 G; 7 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1574 GTTCTGATGTTGATGAAA 1592
 ||||| ||||| ||||| |||||

DB 1 GTCTTGATGTTGATGAAA 19
 RESULT 143
 AAH58297
 ID AAH58297 standard; DNA; 19 BP.
 XX
 AC AAH58297;
 XX
 DT 10-SEP-2001 (first entry)
 DE Cell-cycle dependent kinase cdk7 ribozyme binding site SEQ ID NO:721.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; WMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cystostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US29500.
 XX
 PR 26-OCT-1999; 99US-0161532.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;
 XX
 PS WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using
 CC ribozymes that cleave RNA encoding cytokines involved in inflammation,
 CC matrix metalloproteinases, growth factors and cell-cycle dependent
 CC kinases -
 XX
 PS Example 1; Page 124; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 19 BP; 5 A; 1 C; 4 G; 9 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1574 GTTTCGATTCTATGGAAA 1592
 ||| ||||| ||||| |||||
 Db 1 GTCTTCGATTCTATGGAAA 19

RESULT 144
 ABX93225/c
 ID ABX93225 standard; DNA; 19 BP.
 XX
 AC ABX93225;
 XX
 DT 30-MAY-2003 (first entry)
 XX
 DE PCR primer LP132R used to clone cDNA encoding cotton CYP706B1.
 XX
 KW Cotton; (+)-delta-cadinene 8-hydroxylase; CYP706B1; cytochrome P450;
 KW biosynthesis of gossypol; sesquiterpene; cotton seed; cotton cultivate;
 KW sesquiterpenoid; livestock feed; PCR; primer; ss.
 XX
 OS Gossypium arboreum.
 XX
 PN US2002187538-A1.
 XX
 PD 12-DEC-2002.
 XX
 PP 07-FEB-2002; 2002US-0067534.
 XX
 PR 07-FEB-2001; 2001US-267160P.
 XX
 PA (ESSE/) ESSENBERG M K.
 PA (CHEN/) CHEN X.
 PA (LIOP/) LIU P.
 PA (WANG/) WANG Y.
 XX
 PI Eszenberg MK, Chen X, Luo P, Wang Y;
 XX
 DR WPI; 2003-341036/32.
 XX
 DT Novel cotton (+)-gamma-cadinene 8-hydroxylase polypeptide designated as
 PT CYP706B1, useful as target for suppression of biosynthesis of gossypol
 PT formation in cotton seeds -
 XX
 PS Example 1; Page 4; 26pp; English.

CC The present invention relates to the isolation of cotton
 CC (+)-delta-cadinene 8-hydroxylase (designated as CYP706B1), and the
 CC polynucleotide sequence encoding it. The CYP706B1 protein is
 CC a cytochrome P450 which is useful as a target for suppression of the
 CC biosynthesis of gossypol and related sesquiterpenes in cotton seeds
 CC through genetic engineering techniques. The polynucleotide sequence
 CC encoding CYP706B1 is useful in suppression of the biosynthesis of
 CC gossypol and related sesquiterpenes in cotton seeds, where the
 CC polynucleotide sequence is expressed in antisense or sense orientation
 CC as a perfect match to the native gene whose expression is sought to
 CC be suppressed. The polynucleotide sequence of the invention is useful
 CC for producing cotton cultivars which avoid the presence of
 CC sesquiterpenoids in their seeds, and for producing cotton seed product
 CC which is suitable for use as a feed for both livestock and humans.
 CC The present sequence represents a PCR primer used to clone cDNA
 CC encoding cotton CYP706B1 in the examples of the present invention.
 XX
 SQ Sequence 19 BP; 3 A; 1 C; 8 G; 7 T; 0 other;
 Query Match 1.1%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 563 ACCATGAATATCCAGAAC 581
 ||| ||||| ||||| |||||
 Db 19 ACCATGAATATCCAGAAC 1

RESULT 145
 ABZ10313/c
 ID ABZ10313 standard; DNA; 19 BP.
 XX
 AC ABZ10313;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related primer SEQ ID NO:453.
 XX
 KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200277272-A2.
 XX
 PD 03-OCT-2002.
 XX
 PP 26-MAR-2002; 2002WO-EP03401.
 XX
 PR 26-MAR-2001; 2001US-278333P.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Maier S, Model P, Mueller V, Otto T;
 PI Pellet C, Schwöpe I, Ziebarth H;
 XX
 DR WPI; 2003-018942/01.
 XX

XX Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent
 PT that distinguishes between methylated and non-methylated CpG
 PT dinucleotides -
 XX

XX Claim 11; Page 35; 117pp; English.

CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09661 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related
 CC DNA sequences. The nucleotide sequences from the present invention can
 CC also be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables
 CC a highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients.
 XX

XX SQ Sequence 19 BP; 7 A; 9 C; 0 G; 3 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 476 TGTGGGTCTCTGTAGGGT 494
 ||| ||||| ||||| |||||
 Db 19 TGAGGGATTCTGTAGGGT 1

RESULT 146
AAQ75568/c
ID AAQ75568 standard; DNA; 20 BP.

XX AC AAQ75568;
XX AC

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

PD 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA
followed by digestion with restriction enzymes

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
aggregate of double-stranded cDNAs by using an aggregate of mRNAs
and a plural type of labelled reverse transcription primers
(GENSEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
template for each reverse transcription primer; (b) digesting each of
the prepared aggregates of the double-stranded cDNAs with restriction
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
separate lanes. The method can be used to analyse gene expression
rapidly and easily.

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 615 TACAAAAACACAAATAA 633

DB 20 TACAAAAACAAAAA 2

RESULT 147
AAQ91529/c
ID AAQ91529 standard; DNA; 20 BP.

XX AAQ91529;

DT 22-DEC-1995 (first entry)

XX Tyrosinase gene 3' primer.

XX Restriction fragment length polymorphism; RFLP; point mutation;
KW mapping; primer; polymerase chain reaction; PCR; tyrosinase; ss.

XX Synthetic.

XX CA2136705-A.

XX 27-MAY-1995.

PD

XX 25-NOV-1994; 94CA-2136705.
XX 26-NOV-1993; 93US-0157269.
XX (CLAR-) CLARKE INST PSYCHIATRY.
XX Kennedy JL, Petronis A;
XX WPI; 1995-255407/34.
XX Screening for polymorphism by amplification of pooled nucleic acid
PT - restriction with endonuclease(s), sepn. of fragments and
PT comparison of restriction patterns, for detecting disease related
PT mutation(s), in genetic mapping etc.
XX Example 3; Page 28; 48pp; English.
XX A TaqI polymorphism at the CCAATT box of the human tyrosinase
CC gene was identified by amplification of the 5' promoter region
CC using the primers given in AAQ91528-29, and examination of the
CC restriction patterns of the amplified products.
XX Sequence 20 BP; 4 A; 8 C; 1 G; 7 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 964 TTGTGAGGACATGTGGAG 982

DB 20 TTGTGAGGACTAGAGGAG 2

RESULT 148
AAAT74234
ID AAAT74234 standard; DNA; 20 BP.

XX AAAT74234;

DT 10-FEB-1998 (first entry)

XX Mouse bg critical region YAC STS D13Sf8 reverse primer.

XX Lyst1; mouse; lysosomal trafficking regulator; beige; bg gene;
KW Chediak-Higashi syndrome; CH syndrome; sequence tagged site; STS;
KW D13Sf8; yeast artificial chromosome; YAC; PCR; primer; ss.

XX Synthetic.

XX Mus musculus.

XX WO9728262-A1.

PD 07-AUG-1997.

XX 31-JAN-1997; 97WO-US01748.

XX 23-DEC-1996; 96US-0034346.

XX 01-FEB-1996; 96US-0011146.

XX 20-DEC-1996; 96US-0033599.

XX (UYFL) UNIV FLORIDA.

XX Barbosa-Alleyne MDFS, Kingsmore SF;

XX WPI; 1997-402616/37.

XX Mammalian lysosomal trafficking regulators LYST1, LYST2 and
PT LYST2 - useful to diagnose Chediak-Higashi syndrome

XX Example 1; Page 68; 237pp; English.

XX This oligonucleotide comprises a reverse primer sequence for

ID	AA96384	standard; DNA; 20 BP.
XX	AA96384;	
XX	AA96384;	
XX	13-SEP-1999	(first entry)
XX	PCR primer	used to amplify an ORF of Chlamydia pneumoniae.
DE	Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;	
XX	sinusitis; purulent otitis media; erythema nodosum; pharyngitis;	
KW	vaccine; neutralising epitope; PCR primer; ss.	
KW	Synthetic.	
XX	Chlamydia pneumoniae.	
OS	W09927105-A2.	
XX	03-JUN-1999.	
XX	20-NOV-1998;	98WO-IB01890.
XX	04-NOV-1998;	98US-0107078.
ER	21-NOV-1997;	97FR-0014673.
PR	(GSST) GENSET.	
XX	Griffais R;	
XX	WPI; 1999-357842/30.	
XX	Genome sequence of Chlamydia pneumoniae	
XX	Page 1822; Disclosure; 1912pp; English.	
XX	AA91991-X97517	represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AA91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AA91990-991) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
CC	Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 Other;	
XX	Query Match	1.1%; Score 14.2; DB 1; Length 20;
XX	Best Local Similarity	84.2%; Pred. No. 2.7e+02;
XX	Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	968	GAGGACATCTGGAGCACT 986
DB	19	GAGGATATTGGAGCCCT 1
XX	RESULT 153	
XX	AA915294	
ID	AA915294	standard; DNA; 20 BP.
XX		

XX
XX
DT 29-APR-1999 (first entry)
XX
XX
DE PCR primer RF-S4.
XX
XX thermocstable polypeptide factor; DNA synthesis activity;
KW DNA polymerase; in vitro DNA synthesis; PCR primer; ss.
KW

XX
PN WC9900506-A1.

```

XX 07-JAN-1999.
XX PD
XX PF
XX 24-JUN-1998; 98WO-JP02845.
XX PR
XX 21-NOV-1997; 97JP-0320692.
XX PR
XX 26-JUN-1997; 97JP-0187496.
XX PA
XX (TAKI ) TAKARA SHUZO CO LTD.
XX PI
XX Asada K, Fujita T, Kato I, Miyake K, Mukai H, Sato Y;
XX PI
XX Uemori T;
XX DR
XX WPI; 1999-095751/08.
XX PT
XX Thermostable polypeptide factors promoting the activity of DNA
XX polymerase - for improvement of DNA synthesis and amplification in
XX vitro.
XX PS
XX Example 9; Page 127; 177pp; Japanese.
XX CC
XX The present PCR primer was used in the course of the invention. The
XX specification describes Pyrococcus furiosus thermostable polypeptide
XX factors. These factors bind to, and promote the DNA synthesis activity
XX of DNA polymerase. The polymerase related factors can be used to
XX provide more efficient in vitro DNA synthesis and amplification
XX systems (e.g. for polymerase chain reaction) by using the factors in
XX conjunction with a DNA polymerase.
XX SQ
XX Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 583 TACTATATGTTAAAGTATT 601
DB 1 TTCTGCTATGTTAAAGTATT 19

RESULT 154
AAK15295/C
ID AAK15295 standard; DNA; 20 BP.
XX AC
XX AAK15295;
XX DT
XX 29-APR-1999 (first entry)
XX DE
XX PCR primer RP-S5.
XX KW
XX Thermostable polypeptide factor; DNA synthesis activity;
XX DNA polymerase; in vitro DNA synthesis; PCR primer; ss.
XX OS
XX Synthetic.
XX XX
XX W09900506-A1.
XX PN
XX 07-JAN-1999.
XX PD
XX 24-JUN-1998; 98WO-JP02845.
XX PF
XX 21-NOV-1997; 97JP-0320692.
XX PR
XX 26-JUN-1997; 97JP-0187496.
XX PA
XX (TAKI ) TAKARA SHUZO CO LTD.
XX PI
XX Asada K, Fujita T, Kato I, Miyake K, Mukai H, Sato Y;
XX PI
XX Uemori T;
XX DR
XX WPI; 1999-095751/08.
XX PT
XX Thermostable polypeptide factors promoting the activity of DNA
XX polymerase - for improvement of DNA synthesis and amplification in

```

```

PT vitro.
XX Example 9; Page 128; 177pp; Japanese.
XX CC
XX The present PCR primer was used in the course of the invention. The
XX specification describes Pyrococcus furiosus thermostable polypeptide
XX factors. These factors bind to, and promote the DNA synthesis activity
XX of DNA polymerase. The polymerase related factors can be used to
XX provide more efficient in vitro DNA synthesis and amplification
XX systems (e.g. for polymerase chain reaction) by using the factors in
XX conjunction with a DNA polymerase.
XX CC
XX Sequence 20 BP; 9 A; 4 C; 2 G; 5 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 583 TACTATATGTTAAAGTATT 601
DB 20 TTCTGCTATGTTAAAGTATT 2

RESULT 155
AAA38895
ID AAA38895 standard; DNA; 20 BP.
XX AC
XX AAA38895;
XX DT
XX 25-AUG-2000 (first entry)
XX DE
XX PCR primer SEQ ID NO:24 used in Example 1.
XX KW
XX Replication fork inhibitor protein; amplification; ARS; PCR primer;
XX autonomously replicating sequence; recombinant protein; ss.
XX OS
XX Synthetic.
XX XX
XX W0200022107-A1.
XX PN
XX 20-APR-2000.
XX PD
XX 14-OCT-1999; 99WO-JP05673.
XX PF
XX 15-OCT-1998; 98JP-0292897.
XX PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX (HORI/) HORIUCHI T.
XX PI
XX Horiuchi T, Kobayashi T;
XX DR
XX WPI; 2000-317967/27.
XX PT
XX Amplification of a foreign gene by recombining close to a recombination
XX hot spot and autonomously replicating sequence and culturing in the
XX presence of a replication fork inhibitor protein for efficient foreign
XX gene expression.
XX PS
XX Example 1; Page 48; 66pp; Japanese.
XX CC
XX The present invention describes a method for amplifying a foreign gene
XX which comprises transferring the foreign gene into a host close to a
XX recombination hot spot and an autonomously replicating sequence and
XX culturing it in the presence of a replication fork inhibitor protein.
XX CC
XX The replication fork inhibitor proteins, and vectors containing them,
XX can be used to produce recombinant proteins with increased efficiency.
XX CC
XX AAA38872 to AAA38895 represent PCR primers which are used in an example
XX from the present invention.
XX SQ
XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;

```

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 441 CTTCAAGCAATCTACTTC 459
Db 1 CGTCCATCAATCTACTTC 19

RESULT 156
AAH80900/C
ID AAH80900 standard; cDNA; 20 BP.
XX AC AAH80900;
XX DT 19-SEP-2001 (first entry)
XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 864.
XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX KW disease diagnosis; SS.
XX OS Human immunodeficiency virus type 1.
XX PN US6251588-B1.
XX PD 26-JUN-2001.
XX PF 10-FEB-1998; 98US-0021701.
XX PR 10-FEB-1998; 98US-0021701.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX DR WPI; 2001-424456/45.
XX PT Predicting the potential of an oligonucleotide to hybridize to a target
XX PT nucleotide sequence, useful for evaluating oligonucleotide probe
XX PT sequences, by identifying a oligonucleotides based on the evaluation of
XX PT parameters -
XX PS Example 2; Column 73; 342pp; English.
XX CC The present invention describes a method for predicting the potential of
XX CC an oligonucleotide to hybridize to a (complementary) target nucleotide
XX CC sequence, involving identifying a subset of oligonucleotides within the
XX CC predetermined number of unique oligonucleotides based on the evaluation
XX CC of the parameter. Oligonucleotides in the subset are identified that are
XX CC clustered along a region of the nucleotide sequence that is hybridisable
XX CC to the target nucleotide sequence. This is useful for evaluating
XX CC oligonucleotide probe sequences. The present sequence is an
XX CC oligonucleotide described in the exemplification of the invention.
XX SQ Sequence 20 BP; 9 A; 1 C; 5 G; 5 T; 0 other;
Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 982 GCACCTTAAGTTTTCAT 1000
Db 20 GCACCTTAAGTTTTCCT 2

RESULT 157
AAH80901/C
ID AAH80901 standard; cDNA; 20 BP.
XX AC AAH80901;
XX XX
XX DT 19-SEP-2001 (first entry)
XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 865.

XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX KW disease diagnosis; SS.
XX OS Human immunodeficiency virus type 1.
XX PN US6251588-B1.
XX PD 26-JUN-2001.
XX PF 10-FEB-1998; 98US-0021701.
XX PR 10-FEB-1998; 98US-0021701.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX DR WPI; 2001-424456/45.
XX PT Predicting the potential of an oligonucleotide to hybridize to a target
XX PT nucleotide sequence, useful for evaluating oligonucleotide probe
XX PT sequences, by identifying a oligonucleotides based on the evaluation of
XX PT parameters -
XX PS Example 2; Column 73; 342pp; English.
XX CC The present invention describes a method for predicting the potential of
XX CC an oligonucleotide to hybridize to a (complementary) target nucleotide
XX CC sequence, involving identifying a subset of oligonucleotides within the
XX CC predetermined number of unique oligonucleotides based on the evaluation
XX CC of the parameter. Oligonucleotides in the subset are identified that are
XX CC clustered along a region of the nucleotide sequence that is hybridisable
XX CC to the target nucleotide sequence. This is useful for evaluating
XX CC oligonucleotide probe sequences. The present sequence is an
XX CC oligonucleotide described in the exemplification of the invention.
XX SQ Sequence 20 BP; 9 A; 1 C; 5 G; 5 T; 0 other;
Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 982 GCACCTTAAGTTTTCAT 1000
Db 19 GCACCTTAAGTTTTCCT 1

RESULT 158
AAH80905/C
ID AAH80905 standard; cDNA; 20 BP.
XX AC AAH80905;
XX DT 19-SEP-2001 (first entry)
XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 869.
XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX KW disease diagnosis; SS.
XX OS Human immunodeficiency virus type 1.
XX PN US6251588-B1.
XX PD 26-JUN-2001.
XX PF 10-FEB-1998; 98US-0021701.
XX PR 10-FEB-1998; 98US-0021701.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.

PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 DR WPI; 2001-424456/45.

XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters -

PS Example 2; Column 73; 342pp; English.

XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridizable
 CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.

XX Sequence 20 BP; 10 A; 3 C; 3 G; 4 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 977 TCGAAGCAGCTTAAAGTTT 995
 ||| ||||| ||||| |||||
 DB 20 TGGTTCACCTTAAATTT 2

RESULT 159

AAH80906/c
 ID AAH80906 standard; cDNA; 20 BP.

AC AAH80906;

DT 19-SEP-2001 (first entry)

DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 870.

XX Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.

XX Human immunodeficiency virus type 1.

OS US6251588-B1.

PN 26-JUN-2001.

PD 10-FEB-1998; 98US-0021701.

PF 10-FEB-1998; 98US-0021701.

PR (AGIL-) AGILENT TECHNOLOGIES INC.

PA Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

PI WPI; 2001-424456/45.

XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters -

PS Example 2; Column 73; 342pp; English.

XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are

CC clustered along a region of the nucleotide sequence that is hybridizable
 CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.

XX Sequence 20 BP; 11 A; 3 C; 2 G; 4 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 977 TCGAAGCAGCTTAAAGTTT 995
 ||| ||||| ||||| |||||
 DB 19 TGGTTCACCTTAAATTT 1

RESULT 160

AAH56708
 ID AAH56708 standard; DNA; 20 BP.

AC AAH56708;

DT 06-SEP-2001 (first entry)

DE S. aureus groE operon antisense oligonucleotide SEQ ID NO:356.

XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.

OS Staphylococcus aureus.

PN WO200136625-A2.

PD 25-MAY-2001.

PF 20-NOV-2000; 2000WO-CA01347.

PR 18-NOV-1999; 99US-0166249.

PA (GENE-) GENESENSE TECHNOLOGIES INC.

PI Wright JA, Young AH, Dugourd D;

PS WPI; 2001-355633/37.

PT Novel antisense compounds targeting nucleic acid encoding groEL or
 PT groES gene of microorganism, which hybridize with and inhibit
 PT expression of the genes, useful to inhibit growth of microorganism
 PT having the genes -

PS Claim 3; Page 51; 110pp; English.

XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism. (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL

CC or GS gene and administering (I) such that the growth of microorganism
CC is inhibited. The antisense compounds are utilized for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
CC prevent or delay microbial infections in humans. They are also useful as
CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
CC represent PCR primers for gross sequences which are used in the
CC exemplification of the present invention. AAH56855 to AAH56870 represent
CC groE nucleotide sequence given in the present invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 2 G; 10 T; 0 other;

Query Match 1.1%; Score 14.2; DS 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1566 TTTTACTGTTTCTGATTG 1584
Db 2 TTTTACGCTTCTGATTG 20

RESULT 161
ABQ79871/c
ID ABQ79871 standard; DNA; 20 BP.
XX
AC ABQ79871;
XX
XT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #1.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
XX JP2002191369-A.
XX
XX 09-JUL-2002.
XX
XX 27-DEC-2000; 2000JP-0399573.
XX
XX 27-DEC-2000; 2000JP-0399573.
XX
XX (TOJO) TOYO KOHAN CO LTD.
XX (TAKA/) TAKAHASHI K.
XX WPI; 2002-630904/68.
XX Carrying out a thermal cycle of polymerase chain reaction (PCR) by
XX using a substrate on which a DNA is immobilized used in medical,
XX biochemical, molecular biological and gene engineering fields -
XX Examples; Page 9; 13pp; Japanese.
XX
XX The invention relates to performing a thermal cycle of PCR by using a
XX substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
XX method is useful in the medical, biochemical, molecular biological and
XX genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
XX used in the method of the invention.
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.1%; Score 14.2; DS 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 618 AAAAACAACCAATATTTT 636
Db 19 AAAAACAACCAATATTTT 1

RESULT 162
ABS67672/c

ID XX ABS67672 standard; DNA; 20 BP.
AC XX ABS67672;
DT 29-NOV-2002 (first entry)
XX
DE Casein kinase-2 antisense oligonucleotide ISIS127172.
XX
KW ss; antisense therapy; casein kinase-2 alpha; cytostatic; antidiabetic;
KW antiinflammatory; diabetes; hyperproliferative disorder; cancer; human;
KW breast cancer; prostate cancer; liver cancer; infection; inflammation;
KW tumour; mouse.
XX Homo sapiens.
OS Mus musculus.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /label= OTHER
FT /note= "All cytidines are 5-methylcytidine.
FT Phosphorothioate backbone"
FT 1..5
FT /*tag= b
FT /label= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /label= OTHER
FT /note= "2'-methoxyethyl nucleotides"
XX
XX WO200262818-A2.
XX
XX 15-AUG-2002.
XX
XX 31-JAN-2002; 2002WO-US02942.
XX
XX 08-FEB-2001; 2001US-0780172.
XX (ISIS-) ISIS PHARM INC.
XX McKay R, Freier SM, Wyatt JR;
XX WPI; 2002-627521/67.
XX
XX New antisense oligonucleotides targeted to nucleic acid encoding casein
XX kinase 2-alpha, useful in diagnostic and research applications, or for
XX treating a disease or condition associated with expression of casein
XX kinase 2-alpha -
XX
PS Claim 3; Page 95; 166pp; English.
XX
XX The invention relates to a compound 8-50 nucleobases in length targeted
XX to a nucleic acid molecule encoding casein kinase 2-alpha. The compound
XX specifically hybridises with and inhibits the expression of casein
XX kinase 2-alpha, or specifically hybridises with at least an
XX 8-nucleobase portion of an active site on a nucleic acid molecule
XX encoding casein kinase 2-alpha i.e. an antisense oligonucleotide.
XX Also included are: (1) a composition comprising the compound and a
XX carrier or diluent; (2) inhibiting the expression of casein kinase
XX 2-alpha in cells or tissues by contacting the cells or tissues with the
XX novel compound; and (3) treating an animal having a disease or condition
XX associated with casein kinase 2-alpha by administering to the animal the
XX compound cited above so that expression of casein kinase 2-alpha is
XX inhibited. The antisense compounds are useful for modulating the
XX expression of casein kinase 2-alpha and for treating diseases or
XX conditions associated with expression of casein kinase 2-alpha, e.g.
XX diabetes or hyperproliferative disorder, particularly cancer, such as
XX breast cancer, prostate cancer, or liver cancer. The antisense
XX compounds are also useful for diagnostics, therapeutics, prophylaxis,
XX e.g. to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits, and in distinguishing between functions of
XX various members of a biological pathway. The present sequence is a

CC casein kinase-2 alpha antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 other;
Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 438 AAAGTTCAGCAATCTAC 456
DB 19 AGACTTCAAGCAATGTAC 1
RESULT 163
ABS59257
ID ABS59257 standard; DNA; 20 BP.
AC ABS59257;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CAS gene antisense oligonucleotide, ISIS 128210.
XX
KW Human; ss; antisense; cellular apoptosis susceptibility gene;
KW antiinflammatory; antitumour; cytostatic; CAS; CSE1; CSP;
KW chromosome 20q13; mitosis; apoptosis; proliferation; cancer;
KW importin-alpha; nuclear localisation; cell cycle;
KW hyperproliferative disorder; degenerative disorder; Alzheimer's disease;
KW Parkinson's disease; atrophic lateral sclerosis; ALS;
KW retinitis pigmentosa; blood cell disorder; gene therapy; infection;
KW inflammation; tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /*mod_base= "OTHER"
FT /*note= "OTHER = phosphorothioate backbone, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /*mod_base= "OTHER"
FT /*note= "OTHER = 2'-O-methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= "OTHER"
FT /*note= "OTHER = 2'-O-methoxyethyl nucleotides"
XX
FN WO200246367-A2.
XX
XX 13-JUN-2002.
XX
XX 29-OCT-2001; 2001WO-US51048.
XX
XX 01-NOV-2000; 2000US-0705299.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsett LM, Freier SM;
XX
XX WPI; 2002-608254/65.
XX
XX New antisense compound that hybridizes and inhibits nucleic acid
XX encoding cellular apoptosis susceptibility gene, useful for treating a
XX hyperproliferative disorder such as cancer
XX
XX Claim 3; Page 91; 135pp; English.
XX
XX The invention discloses antisense compounds, of 8 - 50 nucleobases in
XX length, targeted to a nucleic acid molecule encoding a human cellular
XX apoptosis susceptibility gene (CAS or CSE1 or CSP), located on chromosome

CC 20q13. CAS has been implicated in the regulation of mitosis, apoptosis
CC and cellular proliferation and is highly expressed in some cancer cells.
CC CAS has also been shown to mediate export of importin-alpha from the
CC nucleus. Importin-alpha is a nuclear import receptor for nuclear
CC localisation signal-containing proteins and deregulation of importin
CC transport is involved in cell cycle defects. The antisense compounds
CC specifically hybridise with, and inhibit expression of, the gene or
CC specifically hybridise with, an 8 nucleobase portion of its active site.
CC The antisense compounds are useful for inhibiting the expression of a
CC cellular apoptosis susceptibility gene in cells or tissues and for
CC treating an animal having a disease or condition associated with a
CC cellular apoptosis susceptibility gene, where the disease or condition is
CC a hyperproliferative disorder such as cancer, preferably breast or colon
CC cancer, degenerative disorders such as Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), retinitis pigmentosa and
CC blood cell disorders. The compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, as research reagents and kits, for
CC distinguishing functions of various members of a biological pathway, in
CC antisense gene therapy and prophylactically (e.g. to prevent or delay
CC infection, inflammation or tumour formation). The antisense
CC oligonucleotides in ABS59252-ABS59322 are targeted to the human CAS gene.
XX
SQ Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 other;
Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1307 TGAACCTAACCAATCCTAGTT 1325
DB 1 TGAATTAACACUCCAGTT 19
RESULT 164
ABQ62328/c
ID ABQ62328 standard; DNA; 20 BP.
XX
AC ABQ62328;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human syntaxin 4 interacting protein antisense oligonucleotide 67.
XX
KW Human; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
XX WO200224864-A2.
XX
XX 28-MAR-2002.
XX
XX 19-SEP-2001; 2001WO-US29251.
XX
XX 22-SEP-2000; 2000US-0668313.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Wyatt JR;
XX
XX WPI; 2002-401986/43.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
XX molecule encoding Syntaxin 4 interacting protein, useful for treating
XX diabetes, obesity and skeletal muscle disorder
XX
XX Claim 3; Page 84; 154pp; English.
XX
XX The invention comprises antisense oligonucleotides designed to inhibit
XX expression of Syntaxin 4 interacting protein. The antisense
XX oligonucleotides of the invention are useful for inhibiting the

CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC human Syntaxin 4 interacting protein antisense oligonucleotide.
CC NOTE: The present sequence contains a phosphorothioate backbone and
CC 2'-O-methoxyethyl wings.

XX
SQ Sequence 20 BP; 10 A; 1 C; 2 G; 7 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1045 TATTATGATATTATTTAA 1063
DB 19 TATTTCTGATACATTAA 1

RESULT 165
AAS18578
ID AAS18578 standard; DNA; 20 BP.
XX
AC AAS18578;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human translocating chain-associated membrane protein, RT-PCR primer #2.
XX
KW Human; translocating chain-associated membrane protein; BiotRAM;
KW reverse transcriptase PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1310184-A.
XX
PD 29-AUG-2001.
XX
PF 24-FEB-2000; 2000CN-0111729.
XX
PR 24-FEB-2000; 2000CN-0111729.
XX
PA (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
WPI; 2002-034947/05.
XX
PT New human transposition chain related membrane protein and its coding
PT sequence -
XX
PS Example 3; Page 12; 22pp; Chinese.

CC The invention relates to a novel human translocating chain associating
CC membrane protein (BiotRAM), polynucleotides encoding this polypeptide
CC and the recombination process used to produce the polypeptide. The
CC present invention also discloses the method of applying the polypeptide
CC and polynucleotides in treating immunological disorder, malignant tumour,
CC cancer and other diseases. The antagonist resisting the polypeptide and
CC its treatment effect is also disclosed. Diagnosis and determination
CC method based on the discrimination of the mutation in the nucleic acid
CC sequence and the change in the polypeptide expression level, and the
CC application of the polynucleotides encoding the BiotRAM. The present
CC sequence represents a reverse transcriptase (RT)-PCR primer used to
CC isolate the coding sequence of the novel human BiotRAM protein as
CC described in the invention.

XX
SQ Sequence 20 BP; 8 A; 0 C; 1 G; 11 T; 0 other;

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 591 TGTAAAGTATTATTATT 609
DB 2 TTTAAAGTATTATTATT 20

RESULT 166
ACC47011
ID ACC47011 standard; DNA; 20 BP.
XX
AC ACC47011;
XX
DT 05-JUN-2003 (first entry)
XX
DE Mouse phospholipase A2 antisense oligonucleotide SEQ ID NO:108.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Mus musculus.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 1..20 /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5 /tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20 /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"

WO200297133-A1.
XX
PD 05-DEC-2002.
XX
PF 21-MAY-2002; 2002WO-US16135.
XX
PR 25-MAY-2001; 2001US-0865866.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Wyatt JR;
XX
WPI; 2003-140495/13.
XX
PT New compound that hybridizes with and inhibits the expression of
PT Phospholipase A2, group IIA, useful for preparing a composition for
PT treating or preventing inflammation, cancer, psoriasis or diabetes -
XX
PS Claim 3; Page 89; 135pp; English.

CC The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridises with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an
CC animal having a disease or condition associated with phospholipase A2,
CC group IIA (synovial). (I) has antiinflammatory, antidiabetic, cytostatic
CC and antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents a mouse phospholipase A2 group IIA (synovial)

CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention.
 XX Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;
 SQ Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 690 ATTGGGCAAGGCGCAACA 708
 DB 1 ATTGAGCCAAAGGCATGCA 19

RESULT 167
 AAD52331/C
 ID AAD52331 standard; DNA; 20 BP.
 XX AC AAD52331;
 XX DT 02-MAY-2003 (first entry)
 XX DE Human IFNGR2 antisense oligonucleotide, ISIS #142809.
 XX KW Antisense; interferon gamma receptor 2; autoimmune disorder; cancer;
 KW autoimmune thyroiditis; autoimmune insulinitis; multiple sclerosis;
 KW diabetes; autoimmune arthritis; Crohn's disease; apoptosis; IFNGR2;
 KW gene therapy; prophylaxis; human; phosphorothioate; ss.
 XX OS Homo sapiens.
 XX CS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine
 residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 XX WO20028163-A1.
 XX PD 07-NOV-2002.
 XX PF 16-APR-2002; 2002WO-US12007.
 XX PR 26-APR-2001; 2001US-0843377.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Watt AT;
 XX WPI; 2003-156688/15.
 XX DR New antisense oligonucleotides for modulating Interferon gamma receptor
 XX 2, particularly useful for treating autoimmune disorders (e.g. multiple
 XX sclerosis or Crohn's disease), cancers or diseases caused by aberrant
 XX apoptosis
 XX Example 15; Page 86; 127pp; English.
 XX The invention relates to antisense compounds, composition and methods for
 XX modulating the expression of human interferon gamma receptor 2 (IFNGR2).
 XX The compositions comprise antisense compounds targeted to nucleic acids
 XX encoding IFNGR2. Antisense compounds of the invention are useful for
 XX treating diseases or conditions associated with IFNGR2, e.g. autoimmune

CC disorder (e.g. autoimmune thyroiditis, diabetes, multiple sclerosis,
 CC autoimmune arthritis, autoimmune insulinitis or Crohn's disease), cancer,
 CC or a disease/disorder caused by aberrant apoptosis. They are also useful
 CC for diagnostics, therapeutics, prophylaxis or as research reagents or
 CC kits. The invention is useful in gene therapy. The present sequence is
 CC an antisense oligonucleotide targeted to human IFNGR2 DNA.
 XX Sequence 20 BP; 6 A; 2 C; 5 G; 7 T; 0 other;
 SQ Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 437 GAAACTTCAAGCAAACTCA 455
 DB 19 GAAACTTCCAGCATTTCTA 1

RESULT 168
 AAD51486/C
 ID AAD51486 standard; DNA; 20 BP.
 XX AC AAD51486;
 XX DT 16-APR-2003 (first entry)
 XX DE 3' end of the cotton genomic remnant DNA.
 XX KW Insect resistance; MON15985 event; plant breeding; cotton; ds.
 XX OS Gossypium hirsutum.
 XX PN WO2002100163-A2.
 XX PD 19-DEC-2002.
 XX PF 05-JUN-2002; 2002WO-US17853.
 XX PR 11-JUN-2001; 2001US-297406P.
 XX PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX PI Huber SA, Roberts JK, Shappley ZW, Doherty S;
 XX WPI; 2003-148719/14.
 XX Insect resistant cotton plants, tissues and seeds that include the
 XX MON15985 event, useful in plant insect protection and plant breeding
 XX Disclosure; Page 46; 52pp; English.
 XX The invention relates to insect resistant cotton plants, tissues and
 XX seeds that include the MON15985 event. The methods and compositions
 XX of the invention are useful in the field of plant molecular biology,
 XX in particular plant insect protection and plant breeding. The MON15985
 XX event confers resistance to lepidopteran insect damage. The present
 XX sequence is 3' end of the cotton genomic remnant DNA. This sequence
 XX is used in the exemplification of the invention.
 XX Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 other;
 SQ Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1310 ACTAACCAATCCTAGTTTGA 1328
 DB 19 ACCGACACCTACTTTGA 1

RESULT 169
 AAT56320
 ID AAT56320 standard; RNA; 15 BP.

XX AAT56320;
 XX 25-MAR-2003 (updated)
 DT 14-MAY-1997 (first entry)
 XX Mouse TNF-a hammerhead ribozyme target sequence (nt position 1310).
 DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Mus musculus.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB00156.
 PF
 XX 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0281932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR
 XX Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 PT
 XX Claim 2; Page 252; 407pp; English.
 PS
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding

CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
 Query Match 1.1%; Score 14; DB 1; Length 15;
 Best Local Similarity 28.6%; Pred. No. 2.2e+02;
 Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1038 TATTATTATTAT 1051
 Db 1 UUUUUUUUUUU 14
 RESULT 170
 AAT55811
 ID AAT55811 standard; RNA; 15 BP.
 XX
 AC AAT55811;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human TNF-alpha hammerhead ribozyme target sequence (nt position 1269).
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0281932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.

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PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LM;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozyms having modified bases and methods for producing them -
PT for use in inhibiting disease related genes
PS Claim 2; Page 243; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNP-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNP-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
SQ Query Match 1.1%; Score 14; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 2.2e+02;
Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 1038 TATTATTATTATTAT 1051
DB 1 UAUUUUUUUUUU 14

RESULT 171
AAT55796
ID AAT55796 standard; RNA; 15 BP.
AC AAT55796;
XX XX
DT 25-MAR-2003 (updated)
DT 25-MAR-1997 (first entry)
XX XX
DE Human TNP-alpha hammerhead ribozyme target sequence (nt position 1258).
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNP-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS; ss.
XX OS Homo sapiens.
XX XX
XX W09523225-A2.

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XX 31-AUG-1995.
XX 23-FEB-1995; 95WO-1B00156.
XX 30-JAN-1995; 95US-0380734.
XX 23-FEB-1994; 94US-0201109.
XX 29-MAR-1994; 94US-0218934.
XX 04-APR-1994; 94US-0222795.
XX 07-APR-1994; 94US-0224483.
XX 15-APR-1994; 94US-0227958.
XX 15-APR-1994; 94US-0228041.
XX 16-MAY-1994; 94US-0245736.
XX 06-JUL-1994; 94US-0271280.
XX 15-AUG-1994; 94US-0291932.
XX 16-AUG-1994; 94US-0291433.
XX 17-AUG-1994; 94US-0292620.
XX 19-AUG-1994; 94US-0293520.
XX 02-SEP-1994; 94US-0300000.
XX 08-SEP-1994; 94US-0303039.
XX 23-SEP-1994; 94US-0311486.
XX 23-SEP-1994; 94US-0311749.
XX 28-SEP-1994; 94US-0314397.
XX 03-OCT-1994; 94US-0316771.
XX 07-OCT-1994; 94US-0319492.
XX 11-OCT-1994; 94US-0321993.
XX 04-NOV-1994; 94US-0334847.
XX 10-NOV-1994; 94US-0337608.
XX 28-NOV-1994; 94US-0345516.
XX 16-DEC-1994; 94US-0357577.
XX 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LM;
XX Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, McSwiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
XX Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozyms having modified bases and methods for producing them -
PT for use in inhibiting disease related genes
XX Claim 2; Page 242; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNP-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNP-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
SQ Query Match 1.1%; Score 14; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 2.2e+02;
Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 1038 TATTATTATTATTAT 1051
DB 1 UAUUUUUUUUUU 14

RESULT 172

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ABT34305
ID ABT34305 standard; DNA; 16 BP.
XX
AC ABT34305;
XX
DT 12-JUN-2003 (first entry)
XX
DE Hypocretin receptor 1 PCR primer SEQ ID No 91.
XX
KW Eating disorder; polymorphism; dataset; allele; HGBASE identification;
KW serotonin receptor 1D; delta-opioid receptor; dopamine receptor D2;
KW anorexia nervosa; bulimia nervosa; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2003012143-A1.
XX
PD 13-FEB-2003.
XX
PF 16-JUL-2002; 2002WO-US22555.
XX
PR 16-JUL-2001; 2001US-305153P.
XX
PR 20-JUL-2001; 2001US-306440P.
XX
PR 13-NOV-2001; 2001US-331285P.
XX
PR 19-DEC-2001; 2001US-340843P.
XX
PR 19-DEC-2001; 2001US-340844P.
XX
PA (PRIC-) PRICE FOUND LTD.
XX
PI Bergen AW, Yeager M;
XX
DR WPI; 2003-268122/26.
XX
KW New nucleic acid molecule having polymorphisms in the serotonin
PT receptor 1D, delta-opioid receptor, or dopamine receptor D2, useful in
PT diagnostic and prognostic assays for eating disorders, such as anorexia
PT and bulimia nervosa.
XX
PS Example 3; Page 61; 149pp; English.
XX
SS The invention relates to a novel isolated nucleic acid molecule
CC comprising a variant gene associated with an eating disorder and selected
CC from any of 119 polymorphisms with their corresponding genotyping in
CC dataset, alleles and HGBASE identification, given in the specification.
CC The novel nucleic acid molecule has polymorphisms in the serotonin
CC receptor 1D, delta-opioid receptor, or dopamine receptor D2, which is
CC useful in diagnostic and prognostic assays for eating disorders, in
CC particular anorexia nervosa and bulimia nervosa. This polynucleotide
CC sequence represents a hypocretin receptor 1 PCR primer of the invention.
XX
SQ Sequence 16 BP; 3 A; 6 C; 3 G; 4 T; 0 other;

Query Match 1.1%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 877 CCACAGTCTTGT 890
DB 2 CCACAGTCTTGT 15

RESULT 173
AAV97934
ID AAV97934 standard; RNA; 17 BP.
XX
AC AAV97934;
XX
DT 17-MAR-1999 (first entry)
XX
DE Human EGF-R target sequence nucleotide position 5117.
XX
KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;

cancer; genetic drift; detection; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO9833893-A2.
XX
PD 06-AUG-1998.
XX
PF 14-JAN-1998; 98WO-US00730.
XX
PR 04-DEC-1997; 97US-0985162.
PR 31-JAN-1997; 97US-0036476.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PA (UYAS-) UNIV ASTON.
XX
PI Akhtar S, Fell P, McSwiggen JA;
XX
DR WPI; 1998-437449/37.
XX
PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and
PT for treating cancers
XX
PS Claim 5; Page 82; 109pp; English.
XX
SS The present invention describes enzymatic nucleic acid molecules (NAMS)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NAMS can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell.
XX
SQ Sequence 17 BP; 9 A; 1 C; 2 G; 5 U; 0 other;

Query Match 1.1%; Score 14; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.5e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1599 AGTAAATATGAAC 1612
DB 2 AGTAAAUAGAAC 15

RESULT 174
AAZ22807/C
ID AAZ22807 standard; RNA; 17 BP.
XX
AC AAZ22807;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6033.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
KW tuberos sclerosia; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.

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PD 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US06507.
XX
XX 27-MAR-1998; 98US-0079678.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or
XX stability of an mRNA encoding an angiogenic factors
XX
XX Claim 54; Page 243; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with
XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3.
XX
XX Sequence 17 BP; 0 A; 0 C; 3 G; 14 U; 0 other;
XX
XX Query Match 1.1%; Score 14; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1207 AAACAACAAACAA 1220
DB 17 AAACAACAAACAA 4
|||||
|
RESULT 175
AA22808/c
ID AAA22808 standard; RNA; 17 BP.
XX
XX AAA22808;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6034.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

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XX OS Homo sapiens.
XX
XX PN WO9950403-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 24-MAR-1999; 99WO-US06507.
XX
XX PR 27-MAR-1998; 98US-0079678.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or
XX stability of an mRNA encoding an angiogenic factors
XX
XX Claim 54; Page 243; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with
XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3.
XX
XX Sequence 17 BP; 0 A; 0 C; 4 G; 13 U; 0 other;
XX
XX Query Match 1.1%; Score 14; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1207 AAACAACAAACAA 1220
DB 14 AAACAACAAACAA 1
|||||
|
RESULT 176
AA22809/c
ID AAA22809 standard; RNA; 17 BP.
XX
XX AAA22809;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6035.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

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XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 243; 305pp; English.
 XX
 CC The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 4 G; 13 U; 0 other;
 Query Match 1.1%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1207 AAACAACAAACAA 1220
 DB 17 AAACAACAAACAA 4
 RESULT 177
 AA22810/C
 ID AA22810 standard; RNA; 17 BP.
 XX
 AC AAA22810;
 XX
 DT 19-JUN-2000 (first entry);
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6036.

XX Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2, angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 243; 305pp; English.
 XX
 CC The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 4 G; 12 U; 0 other;
 Query Match 1.1%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1207 AAACAACAAACAA 1220
 DB 14 AAACAACAAACAA 1
 RESULT 178
 AAA36306
 ID AAA36306 standard; DNA; 17 BP.
 XX

AAA36306;
26-JUL-2000 (first entry)
Human genomic SNP allele specific oligonucleotide SEQ ID NO:372.
Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
genomic classification; identification; DNA fingerprinting;
tumour characterisation; hybridisation; ss.
Homo sapiens.
WO200018960-A2.
06-APR-2000.
24-SEP-1999; 99WO-US22283.
25-SEP-1998; 98US-0101757.
(MASI) MASSACHUSETTS INST TECHNOLOGY.
Landers JB, Jordan B, Housman DE, Charest A;
WPI; 2000-293181/25.
Detection of single nucleotide polymorphisms in genomes by preparation
and analysis of reduced complexity genomes, useful for genotyping,
fingerprinting and determining allele frequency of SNPs -
Disclosure; Page 64; 11pp; English.
A method has been developed for detecting the presence or absence of a
single nucleotide polymorphism (SNP) allele in a genomic sample. The
method comprises preparing a reduced complexity genome (RCG) from the
genomic sample and analysing the RCG for the presence or absence of a
SNP allele. The method can be used to characterise a tumour, to generate
a genomic pattern for an individual genome or to generate a genomic
classification code for a genome. The method can be used to assess
whether a subject is at risk for developing a disease or to identify a
set of SNP alleles associated with a disease. The method can also be
used to perform linkage analysis. AAA35944 to AAA35947 represent
sequences used in the exemplification of the present invention. AAA35948
to AAA36632 represent nucleotide sequences containing SNPs.
Sequence 17 BP; 12 A; 5 C; 0 G; 0 U; 0 other;
Query Match 1.1%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1207 AAACAAACAAACAA 1220
DB 1 AAACAAACAAACAA 14
RESULT 179
ABN07607
ID ABN07607 standard; DNA; 17 BP.
AC ABN07607;
XX
XX 29-MAY-2002 (first entry)
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7599.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS

PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US16981.
XX 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024283.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-256860P.
XX (ABOM-) ABOICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX
XX Disclosure; SEQ ID 7599; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1, in
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 other;
QY Query Match 1.1%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 939 GCCACCATCTTACC 952
DB 4 GCCACCATCTTACC 17
RESULT 180
ABN07611
ID ABN07611 standard; DNA; 17 BP.

AC ABN07611;
 XX 29-MAY-2002 (first entry)
 DT
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7603.
 DE
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US16981.
 XX
 XX 26-MAY-2000; 2000US-207456P.
 PR
 XX 21-SEP-2000; 2000US-234687P.
 PR
 XX 27-SEP-2000; 2000US-236359P.
 PR
 XX 04-OCT-2000; 2000GB-0024263.
 PR
 XX 30-JAN-2001; 2001WO-US00661.
 PR
 XX 30-JAN-2001; 2001WO-US00662.
 PR
 XX 30-JAN-2001; 2001WO-US00663.
 PR
 XX 30-JAN-2001; 2001WO-US00664.
 PR
 XX 30-JAN-2001; 2001WO-US00665.
 PR
 XX 30-JAN-2001; 2001WO-US00666.
 PR
 XX 30-JAN-2001; 2001WO-US00667.
 PR
 XX 30-JAN-2001; 2001WO-US00668.
 PR
 XX 30-JAN-2001; 2001WO-US00669.
 PR
 XX 30-JAN-2001; 2001WO-US00670.
 PR
 XX 05-FEB-2001; 2001US-266860P.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX
 XX Disclosure; SEQ ID 7603; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX
 XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 other;

Query Match 1.1%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 940 CCACATCTTACCT 953
 DB 1 CCACATCTTACCT 14
 RESULT 181
 AAF24944/C
 ID AAF24944 standard; DNA; 18 BP.
 XX AC AAF24944;
 XX 30-APR-2001 (first entry)
 DT PCR primer used to amplify the human krit1 gene exon 4.
 DE Human; krit1 gene; Ras gene; cavernoma; gene therapy; angiogenesis;
 KW vascular malformation; dysplasia; angiona; tumour; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX FR2795732-A1.
 PN 05-JAN-2001.
 PD 01-JUL-1999; 99FR-0008504.
 PF 01-JUL-1999; 99FR-0008504.
 PR (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX PA Tournier LE, Laberge Le Couteux S, Labauge P;
 PI WPI; 2001-149774/16.
 XX
 XX New primers for amplifying regions of the Krit1 gene, useful for
 PT diagnosis, particularly by detecting mutations, cavernomas, and gene
 PT therapy with this gene -
 XX
 PS Claim 1; Page 16; 39pp; French.
 XX
 CC PCR primers AAF24944-45 were used to amplify exon 4 of the human krit1
 CC gene. Krit1 is a member of the Ras gene family. Mutations in the krit1
 CC gene are responsible for certain vascular abnormalities. The primers are
 CC used to detect mutations in the Krit1 gene, specifically those mutations
 CC that are associated with presence of cavernomas, for diagnosis. The
 CC krit1 gene, or its derivatives, are useful in gene therapy for
 CC controlling or inhibiting angiogenesis, e.g. in cases of vascular
 CC malformation or dysplasia, or angiona, and the Krit1 protein, optionally
 CC modified, may be used similarly, particularly for treatment of tumours.
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 5 G; 13 T; 0 other;
 Query Match 1.1%; Score 14; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 616 ACAAAACACAA 629
 DB 15 ACAAAACACAA 2
 RESULT 182
 AAQ82529/C
 ID AAQ82529 standard; DNA; 20 BP.
 XX AC AAQ82529;
 XX 25-MAR-2003 (updated)
 DT

DT 13-SEP-1995 (first entry)
 XX Chromosome 11 (locus CALCA) STS primer CALCA-A.
 XX sequence sampled mapping; genomic analysis; complex genome mapping;
 XX cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX Synthetic.
 XX WO9423486-A1.
 XX 22-DEC-1994.
 XX 15-JUN-1994; 94WO-US06810.
 XX 15-JUN-1993; 93US-0078471.
 XX 07-SEP-1993; 93US-0117952.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Evans GA, Smith MW;
 XX WPI; 1995-036508/05.
 XX Sequencing complex genomes, present as fragments in a cosmid
 XX library - by sequencing end-specific nucleotides of each clone
 XX then correlating with spatial relationship of cosmid, esp. for
 XX mammalian chromosomes.
 XX Example 4; Page 86; 128pp; English.
 XX Sequences were determined from the ends of chromosome 11-specific
 XX cosmids by automated sequencing without intermediate subcloning.
 XX A sample of 371 DNA sequence fragments were determined and of
 XX these, 277 were suitable for STS primer prediction by computer
 XX analysis (using the "Primer" program available from E. Lander, MIT).
 XX The STSs and cosmids were mapped by in situ hybridisation, somatic
 XX cell hybrid analysis or both. Using this method, 370 STSs specific
 XX for human chromosome 11 were generated and most of them were
 XX regionally mapped. This procedure illustrates a novel method for
 XX sequencing complex genomes, designated "sequence sampled mapping".
 XX The sequence sampled mapping method is useful for the completion of
 XX high density sequence-based maps, and ultimately, for the complete
 XX sequencing of genomic DNA directly from cosmid clones.
 XX See AAQ82001-Q82706 for STS primers. (Also see AAQ91325-58).
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;
 XX Query Match 1.1%; Score 14; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred.No. 2.9e+02;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 389 GTTCCACTGTGCT 902
 XX 17 GTTCCACTGTGCT 4
 XX
 XX RESULT 183
 XX AA96450
 XX ID AA96450 standard; DNA; 20 BP.
 XX
 XX AA96450;
 XX
 XX 13-SEP-1999 (first entry)
 XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 XX vaccine; neutralising epitope; PCR primer; ss.
 XX Synthetic.
 XX OS

OS Chlamydia pneumoniae.
 XX WO9927105-A2.
 XX 03-JUN-1999.
 XX 20-NOV-1998; 98WO-IB01890.
 XX 04-NOV-1998; 98US-0107078.
 XX 21-NOV-1997; 97PR-0014673.
 XX (CEST) GENSET.
 XX Griffais R;
 XX WPI; 1999-357842/30.
 XX Genome sequence of Chlamydia pneumoniae
 XX Page 1827; Disclosure; 1912pp; English.
 XX AAX91991-X97517 represent PCR primers used to amplify open reading
 XX frames and other nucleic acid sequences from the genome of
 XX Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 XX disease such as pneumonia and bronchitis and is thought to be a
 XX contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 XX otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 XX by the open reading frames of the C. pneumoniae genome (see AAX91990-
 XX AAX91999) can be used in immunogenic compositions as vaccines. Vectors
 XX containing C. pneumoniae nucleotide sequences can also be used as
 XX immunogenic compositions, especially where the vector directs the
 XX expression of a neutralising epitope of C. pneumoniae.
 XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;
 XX Query Match 1.1%; Score 14; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred.No. 2.9e+02;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 644 TAAGGATTTTCCTA 657
 XX 7 TAAGGATTTTCCTA 20
 XX
 XX RESULT 184
 XX AA298592
 XX ID AA298592 standard; DNA; 20 BP.
 XX
 XX AA298592;
 XX
 XX 19-JUN-2000 (first entry)
 XX Human MAPK kinase 6 inhibiting antisense oligo ISIS# 101530.
 XX Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense;
 XX sandwich assay; human; ss.
 XX Homo sapiens.
 XX US6033910-A.
 XX 07-MAR-2000.
 XX 19-JUL-1999; 99US-0357073.
 XX 19-JUL-1999; 99US-0357073.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowsett LM;
 XX WPI; 2000-269479/23.
 XX

PT Novel antisense oligonucleotides used for inhibition of
 PT Mitogen-activated protein kinase kinase 6 expression -
 XX Example 15; Column 41; 33pp; English.

XX The invention provides antisense oligonucleotides which are targeted to
 CC a nucleic acid encoding a mitogen-activated protein kinase (MAPK) kinase
 CC 6. The antisense oligonucleotides are used to inhibit MAPK kinase 6
 CC expression, and so are used to treat diseases mediated by MAPK kinase 6
 CC sandwich assays. They may also be used to detect MAPK kinase 6, e.g. in
 CC inhibiting human MAPK kinase 6 mRNA.

XX Sequence 20 BP; 15 A; 3 C; 2 G; 0 U; 0 other;

Query Match 1.13; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 AACCAACAAACAA 1220
 DB 7 AACCAACAAACAA 20

RESULT 185
 AAS13722/C
 ID AAS13722 standard; DNA; 20 BP.

XX AC AAS13722;

XX DT 08-MAY-2002 (first entry)

XX DE Simple sequence repeat, SSR, #19.

XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW cereal profiling; grass profiling; seed batch purity testing.

XX Poae.

XX NZ509193-A.

XX PD 25-MAY-2001.

XX PP 03-JAN-2001; 2001NZ-0509193.

XX PR 24-DEC-1999; 99AU-0004906.

XX PR 04-MAY-2000; 2000AU-0007310.

XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

XX (USC-) UNIV SOUTHERN CROSS.

XX (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.

XX (UTM-) UNIV ADELAIDE.

XX (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

XX Forster JW, Jones ES;

XX WPI; 2001-512563/56.

XX New simple sequence repeats having 2 or more tandemly repeated
 PT nucleotide core elements isolated from ryegrass and fescue, useful for
 PT selecting of genes in grass or cereal breeding or profiling grass or
 PT cereal species varieties -

XX Claim 6; Page 51; 72pp; English.

XX The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for

CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the
 CC breeding, a method for DNA profiling grass or cereal species varieties by
 CC assessing variation between SSR varieties and testing the purity of grass
 CC or cereal seed batches by assessing variation within seed batch of an
 CC SSR. The SSRs may be used in the selection of genes in grass or cereal
 CC breeding, for profiling grass or cereal species varieties, for testing
 CC the purity of grass or cereal seed batches, and for DNA profiling to
 CC establish the distinct identity, uniformity and/or stability of a
 CC cultivar. The present sequence is a ryegrass or fescue SSR.

XX Sequence 20 BP; 0 A; 0 C; 5 G; 15 T; 0 other;

Query Match 1.13; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 AACCAACAAACAA 1220
 DB 20 AACCAACAAACAA 7

RESULT 186
 ABZ01980/C
 ID ABZ01980 standard; DNA; 50 BP.

XX AC ABZ01980;

XX DT 09-JAN-2003 (first entry)

XX DE Human leukocyte gene expression profiling probe SEQ ID NO 1971.

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
 KW probe; ss.

XX OS Homo sapiens.

XX FN W0200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US47856.

XX PR 20-OCT-2000; 2000US-241994P.

XX PR 08-JUN-2001; 2001US-296764P.

XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX PI Ly N, Woodward R, Quattermost T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides -

XX Claim 1; Page 389; 2038pp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,

XX AAA19037;
 AC 19-JUN-2000 (first entry)
 DT Human TIE-2 substrate sequence SEQ ID NO:2263.
 DE
 XX
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytototoxic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX WO9950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 PF
 XX Claim 56; Page 132; 305pp; English.
 PS
 XX The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 XX Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;
 SQ
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1590 AAATATAAAGTAATA 1606
 DB 17 AAATATACAAAGTCAATA 1

RESULT 190
 AAA21468/c
 ID AAA21468 standard; RNA; 17 BP.
 XX
 XX AAA21468;
 AC
 XX 19-JUN-2000 (first entry)
 DT
 XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4694.
 DE
 XX
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytototoxic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX WO9950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 PF
 XX Claim 55; Page 210; 305pp; English.
 PS
 XX The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 XX Sequence 17 BP; 9 A; 0 C; 0 G; 8 U; 0 other;
 SQ

Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 TTATAGTAAATTTATT 1149
 DB 17 TTATATAAATTTATT 1

RESULT 191
 AAA21475/c
 ID AAA21475 standard; RNA; 17 BP.
 XX
 AC AAA21475;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4701.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleros; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 55; Page 210; 305pp; English.

The present invention describes enzymatic cleavage of nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT, and AA17168 to AA17560 and AA17623 to AA17684 represent their corresponding target sequences; AA17685 to AA18385 and AA19087 to AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086 and AA19155 to AA19222 represent their corresponding target sequences; AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and AA21596 to AA21688 represent their corresponding target sequences; AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to AA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

XX SQ Sequence 17 BP; 5 A; 1 C; 3 G; 8 U; 0 other;
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 539 AAACAATGATAGTTT 555
 DB 17 AAACAATGATAGTTT 1

RESULT 192
 AAA22904/c
 ID AAA22904 standard; RNA; 17 BP.
 XX
 AC AAA22904;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6130.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleros; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 249; 305pp; English.

The present invention describes enzymatic cleavage of nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT, and AA17168 to AA17560 and AA17623 to AA17684 represent their corresponding target sequences; AA17685 to AA18385 and AA19087 to AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086 and AA19155 to AA19222 represent their corresponding target sequences; AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and AA21596 to AA21688 represent their corresponding target sequences; AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to AA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as

CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1045 TATTATGATTTATT 1061
 DB 17 TAAATTATTTATT 1
 RESULT 193
 AAV91422/C
 ID AAV91422 standard; RNA; 17 BP.
 XX AC AAV91422;
 XX 18-FEB-1999 (first entry)
 DT Human C-raf target site nucleotide position 2967.
 XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
 XX Homo sapiens.
 OS
 XX WO9850530-A2.
 PN 12-NOV-1998.
 PD
 XX 05-MAY-1998; 98WO-US09249.
 PF 19-DEC-1997; 97US-0068212.
 PR 09-MAY-1997; 97US-0046059.
 PR 09-JUN-1997; 97US-0049002.
 PR 03-JUL-1997; 97US-0051718.
 PR 22-AUG-1997; 97US-0056808.
 PR 02-OCT-1997; 97US-0061121.
 PR 02-OCT-1997; 97US-0061324.
 PR 05-NOV-1997; 97US-0064866.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
 PI Karpelsky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
 PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
 XX WPI; 1999-009494/01.
 DR Identifying new catalytic nucleic acid that modulates selected
 XX processes especially ribozymes that cleave Raf RNA for treating
 PT cancer, restenosis, and also new ribozymes and modified nucleoside
 PT triphosphates used as antiviral agents and synthons
 XX Claim 177; Page 154; 259pp; English.
 PS A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules
 CC with endonuclease activity and catalytic activity, from the present

CC invention, are used to modulate gene expression in plant and mammalian
 CC cells and to cleave target nucleic acid, particularly for treating
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
 CC psoriasis, non-hepatic ascites and infection. They may also be used to
 CC detect genetic drift and mutations in diseased cells and to determine
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.
 XX
 SQ Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1137 ACTAAATTTATTTATT 1153
 DB 17 ATTAATTTATTTATT 1
 RESULT 194
 AAF02426/C
 ID AAF02426 standard; DNA; 17 BP.
 XX AC AAF02426;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #721.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS
 XX WO2000061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US09721.
 PR 12-APR-1999; 99US-0129390.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 72; 164pp; English.
 PS The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the T2 Orphan receptor, EAF3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
 CC protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX Sequence 17 BP; 4 A; 0 C; 3 G; 10 T; 0 other;
 SQ Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1204 ATTAACCAACAAACA 1220
 ||||| ||||| ||||| |||||
 Db 17 ATTATACATACAAACA 1

RESULT 195
 AAA25364
 ID AAA25364 standard; DNA; 17 BP.
 XX
 AC AAA25364;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE
 KW Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1862.
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US08547.
 XX
 PR 20-APR-1998; 98US-0082404.
 PR 23-JUN-1998; 98US-0103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 XX
 PT New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -
 XX
 PS Claim 77; Page 77; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 17 BP; 6 A; 1 C; 3 G; 7 T; 0 other;
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1538 AAGATGTTTATGTGTC 1554
 ||||| ||||| ||||| |||||
 Db 1 AAGTITTTATGTGTCAT 17

Db 1 AAAAGTTTTTATGTGC 17
 ||||| ||||| ||||| |||||

RESULT 196
 AAA25367
 ID AAA25367 standard; DNA; 17 BP.
 XX
 AC AAA25367;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE
 KW Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1865.
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US08547.
 XX
 PR 20-APR-1998; 98US-0082404.
 PR 23-JUN-1998; 98US-0103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 XX
 PT New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -
 XX
 PS Claim 77; Page 77; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 3 G; 8 T; 0 other;
 Query Match 1.1%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1541 AGCTTTTATGTGTCCT 1557
 ||||| ||||| ||||| |||||
 Db 1 AAGTITTTATGTGTCAT 17

RESULT 197

AA25990/c
ID AAA25990 standard; DNA; 17 BP.

XX AC AAA25990;
XX DT 19-JUL-2000 (first entry)
XX DE
XX KW Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2488.
XX KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX KW gene expression modification; cancer; phosphorothioate; endonuclease;
XX KW anticancer; breast cancer; endometrium cancer; ss.

XX OS Homo sapiens.

XX PN WO9954459-A2.

XX PD 28-OCT-1999.

XX PF 19-APR-1999; 99WO-US08547.

XX PR 20-APR-1998; 98US-0082404.

XX PR 23-JUN-1998; 98US-0103636.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
XX PI Matulic-Adamic J;
XX WPI; 2000-013248/01.

XX PT New nucleic acids that interact, and optionally cleave, target
XX PT sequences, used to treat cancer -
XX PS Claim 77; Page 97; 148pp; English.

XX CC The present invention describes nucleic acids (A) that interact stably
XX CC with a target sequence and contain at least one phosphorodithioate
XX CC link, having endonuclease activity. (A), and more generally any
XX CC catalytic nucleic acid (A') that modulates expression of the oestrogen
XX CC receptor gene, are used to treat cancer (particularly of breast or
XX CC endometrium), in vivo or by transforming cells ex vivo and implanting
XX CC treated cells, or for other conditions associated with levels of
XX CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX CC can also be used to correlate inhibition of gene expression with
XX CC alterations in phenotype, particularly for identification of therapeutic
XX CC targets, and as research reagents (for RNA, in the same way that
XX CC restriction endonucleases are used with DNA). The combination of
XX CC modifications in (A) improves resistance to nucleases, binding affinity
XX CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX CC their corresponding target sequences. AAA26219 to AAA26271 represent
XX CC other ribozyme sequences and antisense oligonucleotides used in the
XX CC exemplification of the present invention.

XX SQ Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1055 TTATTATTAGCATCAAA 1071

DB 17 TTATTATTGACATCAAA 1

RESULT 198

ABV80684/c
ID ABV80684 standard; DNA; 17 BP.

XX AC ABV80684;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 1930.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX KW human testis expressed Patched like protein; testis; adrenal; liver;
XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EPI229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-0001167.

XX PR 30-JAN-2001; 2001WO-US00663.

XX PR 30-JAN-2001; 2001WO-US00664.

XX PR 30-JAN-2001; 2001WO-US00665.

XX PR 30-JAN-2001; 2001WO-US00667.

XX PR 30-JAN-2001; 2001WO-US00668.

XX PR 23-MAY-2001; 2001US-0864761.

XX PR 09-OCT-2001; 2001US-0327898.

XX PA (ABOM-) ABOMICA INC.

XX PI Zhan J;

XX WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL),
XX PT useful for identifying agonist and antagonist and specific binding
XX PT partners, and for treating subjects having defects in HTPL -
XX PS Example 2; Page 316; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
XX CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
XX CC has two isoforms, with a few single base pair differences between the
XX CC two. One of the single base pair changes introduces a premature stop
XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX CC shares an overall structure organisation with the Patched protein. The
XX CC shared structural features strongly imply that HTPL plays a role similar
XX CC to that of Patched, and is a potential tumour suppressor. HTPL is
XX CC important in regulating male germ cell development, and the HTPL gene was
XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX CC useful for diagnosing a disorder caused by mutation in HTPL, and in
XX CC therapy and manufacture of a medicament for treatment or prevention of
XX CC such disorder associated with decreased expression or activity of human
XX CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX CC clinically useful diagnostic markers and potential therapeutic agents for
XX CC male infertility and cancer. The present oligonucleotide was used in an
XX CC example from the invention.

XX SQ Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1456 TGTTTATTATGTACAAA 1472

DB 17 TGCTTATGATGTACAAA 1

	RESULT 199	
ABK57491	ABK57491 standard; RNA; 17 BP.	
XX AC	ABX57491;	
XX DT	02-JUL-2002 (first entry)	
XX DE	Human CLCA1 gene enzymatic nucleic acid #1862.	
XX KW	Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.	
OS OS	Homo sapiens.	
XX WN	WO200211674-A2.	
XX PD	14-FEB-2002.	
XX PF	09-AUG-2001; 2001WO-US24970.	
XX PR	09-AUG-2000; 2000US-224383P.	
XX FA	(RIBO-) RIBOZYME PHARM INC.	
XX FA	(SYNT.) SYNTEX USA LLC.	
XX FA	{THOM/) THOMPSON J.	
XX PI	Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE; Grupe A;	
XX DR	WPI; 2002-217145/27.	
XX PT	Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma - Claim 4; Page 114; 152pp; English.	
CC CC	The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention.	
XX SQ	Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other; Query Match 1.1%; Score 13.8; DB 1; Length 17; Best Local Similarity 35.3%; Pred. No. 2.7e+02; Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0	
OY	1134 TATAGTAATTATTTT 1150	
DB	: : : :::	
	1 UAUAUAAAUUUUUU 17	
	RESULT 200	

KW increase; control; form; length; primer; RT-PCR;
 reverse transcriptase; polymerase chain reaction; ss.

OS Synthetic.

XX JP09056382-A.

XX PD 04-MAR-1997.

XX PF 24-AUG-1995; 95UP-0216187.

XX PR 24-AUG-1995; 95JP-0216187.

XX PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

XX PA (CHIK-) ZH CHIKYU KANKYO SANGYO GJOITSU KENKYU.

XX XX WPI; 1997-206629/19.

XX PT DNA encoding plant morphogenesis regulatory protein - useful to
 yield plants with short stems or altered inflorescence

XX PS Example; Page 15; 17pp; Japanese.

XX CC The present sequence is a RT-PCR primer for a mRNA encoding an
 Arabidopsis thaliana plant morphogenesis regulatory protein (MRP),
 which can be used to yield a plant with, e.g. short stems or
 altered inflorescence. The MRP acts on a plant at a specific site
 for a specific period, and can therefore be used to regulate
 extraneous gene expression in a plant. The MRP's cDNA or genomic
 DNA can be used to transform a plant to increase its MRP
 expression, and therefore control the form (particularly stem
 length) of the plant.

XX SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. NO. 2.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1498 GACTGCAATTTTAAATA 1514

DB 17 GACTGCGTTTATAGATA 1

RESULT 202

ID AAX09459/c

XX AAX09459 standard; DNA; 18 BP.

XX AC AAX09459;

XX DT 24-MAR-1999 (first entry)

XX DE Human biallelic polymorphic marker upstream primer #339.

XX KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KW treatment; marker; primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9820165-A2.

XX PD 14-MAY-1998.

XX PF 05-NOV-1997; 97WO-US20313.

XX PR 06-NOV-1996; 96US-0030455.

XX PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.

XX PI Hudson T, Lander ES, Wang D;

XX DR

WPI; 1998-286974/25.

XX XX New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease

XX PS Claim 15; Page 93; 310pp; English.

XX CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the
 CC isolation of various biallelic polymorphic markers found in the human
 CC genome (represented in AAX10269-X12937). These primers can be used in a
 CC method for determining polymorphic forms in an individual for use in
 CC e.g. forensics, paternity testing or for phenotypic typing for diseases,
 CC such as squamaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
 CC muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
 CC hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Shivers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases.

XX SQ Sequence 18 BP; 6 A; 7 C; 4 G; 1 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. NO. 2.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 883 GTCCTTGTTCACCTGTG 899

DB 18 GTCCTTGTGTGCACTGTG 2

RESULT 203

AAX17951

ID AAV17951 standard; DNA; 18 BP.

XX AC AAV17951;

XX DT 29-JUL-1998 (first entry)

XX DE Chlamydia genus specific 16S rRNA sense primer.

XX KW PCR; primer; amplification; endocervical; cloacal; sputum; 16S rRNA; ss.

XX OS Synthetic.

XX OS Chlamydia sp.

XX PN WO9810101-A1.

XX PD 12-MAR-1998.

XX PF 04-SEP-1997; 97WO-US15556.

XX PR 05-SEP-1996; 96US-0025509.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX XX Fields BF, Messmer TO, Skelton SK;

XX XX WPI; 1998-193643/17.

XX DR Detection and differentiation of Chlamydia species - C. pneumoniae,
 PT C. psittaci, and C. trachomatis, using species-specific primers
 PT complementary to the 16S rRNA gene

XX PS Examples; Page 19; 32pp; English.

XX The invention provides a novel assay for detecting and differentiating
 CC Chlamydia pneumoniae, C. psittaci and C. trachomatis in the same sample
 CC at the same time without losing its sensitivity and specificity. This
 CC is made possible by the usage of three 16S rRNA species specific primers
 CC pairs (AAV17933-V17956). The optional first step subjects the test
 CC sample to a PCR reaction which uses the Chlamydia genus specific 16S rRNA
 CC sense and antisense (AAV17952) primers to amplify the generic 16S rRNA
 CC region common to the Chlamydia species. The 436 bp PCR product is then
 CC subjected to another PCR reaction with the species specific primers.
 CC The type of Chlamydia species present or absent is indicated by the
 CC length of the PCR product. A 412 bp product would indicate C. pneumoniae
 CC C. trachomatis presence, a 221 bp product would indicate C. psittaci. These primers can also
 CC and a 127 bp product would indicate C. psittaci. The assay can be used to equally
 CC be used as species specific probes. The assay can be used to equally
 CC identify e.g. C. trachomatis from endocervical swab samples, C. psittaci
 CC from cloacal swab samples from birds and C. pneumoniae from sputum
 CC samples.

XX Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 other;
 SQ Query Match 1.1%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1379 ACAGGAATATGACTTCG 1395
 DB |||||
 1 ACAGGAATATGACTTCG 17

RESULT 204
 AAZ75038
 ID AAZ75038 standard; DNA; 18 BP.
 AC AAZ75038;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker downstream amplification primer SEQ ID NO:9394.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB00822.
 PF 21-APR-1998; 98US-0082614.
 PR 23-NOV-1998; 98US-0109732.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome -
 PS Claim 8; Page 2233; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other

CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.

XX Sequence 18 BP; 0 A; 6 C; 3 G; 9 T; 0 other;
 SQ Query Match 1.1%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 895 CTGNGCCTTCGTTCTC 911
 DB |||||
 2 CTGNGCCTTCGTTCTC 18

RESULT 205
 AAZ75043
 ID AAZ75043 standard; DNA; 18 BP.
 AC AAZ75043;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker downstream amplification primer SEQ ID NO:9399.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB00822.
 PF 21-APR-1998; 98US-0082614.
 PR 23-NOV-1998; 98US-0109732.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome -
 PS Claim 8; Page 2234; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other

CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3357, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 18 BP; 0 A; 6 C; 3 G; 9 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 895 CTGTCCTTGTTTC 911
DB 2 CTGTCCTTGTTTC 18

RESULT 206
AAH86606 standard; DNA; 18 BP.
XX
AC AAH86606;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 2 kinase hammerhead ribozyme recognition site #37.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-0110954.
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1
XX
PS Example 1; Page 18; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
XX
SQ Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 TTTATTAGAGATTTC 1188
DB 18 TTTATTAGAGATTTC 2

RESULT 207
AAD17639/c

ID AAD17639 standard; DNA; 18 BP.
XX
AC AAD17639;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human GCPII gene exon-4 amplifying PCR primer #2.
XX
KW Human; glutamate carboxypeptidase II; GCPII gene; dietary folate; FGCP;
KW folypoly-gamma-glutamate carboxypeptidase; hyperhomocysteinaemia;
KW cardiovascular disease; Alzheimer's disease; neural tube defect;
KW congenital heart defect; colon cancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200168897-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07880.
XX
PR 13-MAR-2000; 2000US-0188983.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Halsted CH, Devlin AM;
XX
DR WPI; 2001-582462/65.
XX
PT Screening an individual for increased risk of low folate status,
PT comprises detecting mutation in human glutamate carboxypeptidase II
PT gene which affects ability of hydrolyzing terminal glutamates from
PT dietary folates -
XX
PS Example 5; Page 26; 38pp; English.
XX
XX The patent discloses methods for screening an individual for increased
CC risk of low folate status. The method involves detecting a mutation
CC in the human glutamate carboxypeptidase (GCP) II gene in a biological
CC sample from said individual, wherein detection of the mutation is
CC indicative of decreased ability of an individual to hydrolyse terminal
CC glutamate residues from dietary folates by folypoly-gamma-glutamate
CC carboxypeptidase (FGCP), a product of GCPII gene. The decreased ability
CC is associated with low folate status. The method is useful for screening
CC an individual for increased risk of low folate status and conditions
CC associated with hyperhomocysteinaemia, cardiovascular disease, colon
CC cancer and altered cognition in the elderly including Alzheimer's
CC disease. Pregnant women with low folate status are at increased risk
CC of bearing children with neural tube defects and congenital heart
CC defects. The present DNA sequence is a PCR primer which is used for
CC amplifying exon-4 of GCPII gene. This primer is designed from PSMA
CC genomic sequence and is used for detecting a mutation in GCPII gene.
XX
SQ Sequence 18 BP; 2 A; 2 C; 3 G; 11 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 767 GCATCATATAAATGA 783
DB 18 GCAACAAATATAAATGA 2

RESULT 208
AAH61772/c
ID AAH61772 standard; DNA; 18 BP.
XX
AC AAH61772;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc 2 kinase hammerhead ribozyme recognition site SEQ ID NO:4196.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulvar;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Disclosure; Page 378; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;
 SQ Query Match 1.1%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2.9e-02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1172 TTTATTAGATAAATTC 1188
 |||||
 DB 18 TTTATTAGATAAATTC 2
 RESULT 209
 ABZ10595
 ID ABZ10595 standard; DNA; 18 BP.
 XX AC ABZ10595;
 XX

DT 16-JAN-2003 (first entry)
 XX Haematopoietic cell proliferation disorder related oligonucleotide #735.
 DE Human; haematopoietic cell proliferation disorder; cytostatic;
 XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200277272-A2.
 XX 03-OCT-2002.
 XX 26-MAR-2002; 2002WO-EP03401.
 XX 26-MAR-2001; 2001US-278333P.
 XX (EPIG-) EPIGENOMICS AG.
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 PI Pelet C, Schwope I, Ziebarth K;
 XX WPI; 2003-018942/01.
 XX Detecting and differentiating between hematopoietic cell proliferative
 XX disorders, comprises contacting a target nucleic acid with a reagent
 PT that distinguishes between methylated and non-methylated CpG
 PT dinucleotides -
 XX Claim 15; Page 52; 117pp; English.
 XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. AB209861 to AB21118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used; for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related
 CC DNA sequences. The nucleotide sequences from the present invention can
 CC also be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables
 CC a highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients.
 XX Sequence 18 BP; 3 A; 1 C; 4 G; 10 T; 0 other;
 SQ Query Match 1.1%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 2.9e-02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1286 TTGTTTATCGAATTT 1302
 |||||
 DB 1 TTGTTTATCGAATTT 17
 RESULT 210
 AAQ47991
 ID AAQ47991 standard; DNA; 19 BP.
 XX

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AC AAQ47991;
XX
XX
DT 25-MAR-2003 (updated)
DT 22-MAR-1994 (first entry)
XX
XX PCR primer used in diagnosis of cystic fibrosis.
DE
XX Cystic fibrosis; mutation; detection; primer; primer set;
KW diagnosis; PCR; polymerase chain reaction; ss.
XX
XX Synthetic.
XX
XX WO9318177-A1.
XX
XX 16-SEP-1993.
XX
XX 11-MAR-1993; 93WO-US02259.
XX
XX 13-MAR-1992; 92US-0850703.
XX
XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX
XX Fortina P, Surrey S;
XX
XX WPI; 1993-303489/38.
XX
XX Diagnosis of cystic fibrosis - using allele specific multiplex
PT polymerase chain reaction system
PT
XX
XX Claim 6; Page 24; 38pp; English.
XX
XX Two primer sets are used for detecting at least two mutations
CC characteristic of cystic fibrosis, each set comprises two primer
CC pairs; pair P1 comprises a primer specific for a normal allele and
CC pair P2 comprises a primer specific for a mutant allele, each pair
CC further comprises a common primer. PCR is performed on genomic DNA
CC using both primer sets simultaneously. Detection of a PCR product
CC of a primer specific for a mutant allele indicates the likelihood
CC that the patient carries a mutation characteristic of the cystic
CC fibrosis phenotype. This primer is designated G551D-N and is the
CC primer specific for the normal allele. (For primers used alongside
CC this primer see AAQ47990 and AAQ47992)
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 other;
SQ
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1435 AATTCTGCTGCTGA 1451
DB 2 AATTCTGCTGCTGA 18

RESULT 211
AAQ62249/c
ID AAQ62249 standard; DNA; 19 BP.
XX
XX AAQ62249;
XX
XX 25-MAR-2003 (updated)
DT 21-NOV-1994 (first entry)
XX
XX Ligase Chain Reaction - specific probe for CF mutation detection.
DE
XX Cystic Fibrosis; CF missense mutation; improved method;
KW diagnosis; known mutation; Ligase chain reaction; G551D; ss.
XX
XX Synthetic.
XX
XX WO9408047-A1.
XX

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PD 14-APR-1994.
XX
XX 07-SEP-1993; 93WO-US08359.
XX
XX 25-SEP-1992; 92US-0951495.
XX
XX (ABSO ) ABBOTT LAB.
XX
XX Beaudet AL, Bouma SR, Fang P, Gordon J, Hsieh W;
PI You T;
XX
XX WPI; 1994-135607/16.
XX
XX Improved ligase chain reaction with high monovalent cation
PT concns., mismatched probes and/or high initial mixing tempa -
PT used to detect small mutations in known DNA sequences, pref. for
PT detecting cystic fibrosis mutations
XX
XX Claim 24; Page 13; 64pp; English.
XX
XX The Ligase Chain Reaction has been improved to increase the
CC "flexibility" or "dynamic range" of each probe set used in the
CC detection of small mutations (single base deletions, insertions and
CC changes, as well as multiple mutations where the size of the
CC mutation is less than about 15% of the average probe length).
CC Previously the determination of the genetic constituency of an
CC individual has been time consuming. The invention comprises reacting
CC probes and sample (suspected to contain the target nucleic acid)
CC under hybridising conditions that have been modified - 1. the
CC concentration of monovalent cation (Na+, K+, or NR3H+, R = H or
CC lower alkyl) is 100-200mM; 2. a "hot start" (temp. range 50-95
CC degree C) may be used; and 3. one of the downstream probes has a
CC mismatch within 5 bases from the 5' end so it is not complementary
CC to the target sequence (The complementary probe is also mismatched).
CC These may be used either on their own or in conjunction.
CC AAQ62245 and AAQ62246 are used to detect the G551D mutation in
CC cystic fibrosis. The remaining probes are selected from AAQ62247-50.
CC This invention is also applicable to other disease related
CC mutations.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 8 A; 4 C; 3 G; 4 T; 0 other;
SQ
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1435 AATTCTGCTGCTGA 1451
DB 18 AATTCTGCTGCTGA 2

RESULT 212
AAQ62250
ID AAQ62250 standard; DNA; 19 BP.
XX
XX AAQ62250;
XX
XX 25-MAR-2003 (updated)
DT 21-NOV-1994 (first entry)
XX
XX Ligase Chain Reaction - specific probe for CF mutation detection.
DE
XX Cystic Fibrosis; CF missense mutation; improved method;
KW diagnosis; known mutation; Ligase chain reaction; G551D; ss.
XX
XX Synthetic.
XX
XX WO9408047-A1.
XX
XX 14-APR-1994.
XX
XX 07-SEP-1993; 93WO-US08359.
XX

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XX PI Cole JL, Kuo LC, Olsen DB;
XX DR WPI; 1997-052364/05.
XX PT Detection of influenza virus endonuclease in a sample - by cleavage
XX PT of an RNA substrate to generate a primer for a labelled polymerase
XX PT extension reaction
XX PS Claim 6; Page 12; 28pp; English.
XX PS This sequence represents the 5' end of Alfalfa Mosaic virus 4 RNA.
XX CC This sequence was used as a substrate for influenza endonuclease in
XX CC the method of the invention. The method allows detection of influenza
XX CC endonuclease activity in a sample and comprises: (a) adding an influenza
XX CC endonuclease substrate to a sample to generate an RNA product; (b)
XX CC hybridising the RNA prod. with a DNA template which comprises a first
XX CC segment complementary to the RNA and a 5' extension of at least one
XX CC nucleotide attached to the 5' end of the DNA segment, such that a
XX CC DNA:RNA hybrid is formed; (c) adding a DNA polymerase and labelled
XX CC mononucleotides such that the DNA polymerase incorporates the
XX CC mononucleotides to the 3' end of the RNA in the RNA:DNA duplex; and
XX CC (d) measuring the amount of labelled hybrid prod. as a measure of the
XX CC amount of influenza endonuclease activity. The method is used to
XX CC quantitate the amount of influenza endonuclease by cleaving the RNA
XX CC substrate which then forms a primer for extension by a DNA polymerase
XX CC on a template. The assay does not involve an electrophoresis step and
XX CC thus may be run in a 96-well microtitre plate. The assay also monitors
XX CC substrate cleavage at the correct position thereby discriminating
XX CC against non-specific cleavage products.
XX SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTATATTTTACTTT 1537
DB 2 UUUUUAUUUUUAUUU 18

RESULT 215
AAT47269
ID AAT47269 standard; RNA; 19 BP.
XX AC AAT47269;
XX DT 28-AUG-1997 (first entry)
XX DE Capped RNA influenza endonuclease substrate #3.
XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX KW endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*mod_base= triphosphorylated
XX FT modified_base 2 /*tag= b
XX FT /*mod_base= 2'-O-methyluridine
XX FT modified_base 13 /*tag= c
XX FT /*mod_base= 2'-deoxyadenosine
XX PN WO9640159-A1.
XX XX 19-DEC-1996.
XX PD 03-JUN-1996; 96WO-US08394.
XX PF

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XX 07-JUN-1995; 95US-0480068.
XX PA (MERI ) MERCK & CO INC.
XX PI Benseler F, Cole JL, Kuo LC, Olsen DB;
XX XX WPI; 1997-051868/05.
XX PT Production of capped RNA or analogues - useful as substrates for
XX PT influenza virus associated virally encoded endonuclease
XX PS Claim 18; Page 13; 39pp; English.
XX XX AAT47264-74780 represent capped RNA molecules produced by the method of
XX CC the invention. The method of the invention is for producing capped RNA
XX CC or RNA analogues. The method comprises reacting a RNA or analogue
XX CC oligonucleotide with a phosphate addition agent to form a RNA or
XX CC analogue mono-, di- or triphosphate, which is then capped. The presence
XX CC of the cap is important for mRNA maturation, initiation of translation,
XX CC and protects the mRNA against various RNases present in the cell. The
XX CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
XX CC treating or preventing an influenza infection in an animal. The synthetic
XX CC capped RNA are substrates for virally encoded endonuclease associated
XX CC with influenza virus. The short non-extendible (due to their length or
XX CC because of the modification of the 3' end of the oligo) RNA molecules are
XX CC potent inhibitors of the cleavage of capped RNA by influenza
XX CC endonuclease. They may be used to investigate viral and cellular
XX CC mechanisms of transcription/translation, or mRNA maturation.
XX SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTATATTTTACTTT 1537
DB 2 UUUUUAUUUUUAUUU 18

RESULT 216
AAT47270
ID AAT47270 standard; RNA; 19 BP.
XX AC AAT47270;
XX DT 28-AUG-1997 (first entry)
XX DE Capped RNA influenza endonuclease substrate #4.
XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX KW endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*mod_base= triphosphorylated
XX FT modified_base 2 /*tag= b
XX FT /*mod_base= 2'-O-methyluridine
XX FT modified_base 13 /*tag= c
XX FT /*mod_base= 2'-deoxy-2'-fluoro-adenosine
XX PN WO9640159-A1.
XX XX 19-DEC-1996.
XX PD 03-JUN-1996; 96WO-US08394.
XX PF

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PR 07-JUN-1995; 95US-0480068.
XX (MERI ) MERCK & CO INC.
XX Benseler F, Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-051868/05.
XX Production of capped RNA or analogues - useful as substrates for
FT Influenza virus associated virally encoded endonuclease
XX Claim 18; Page 13; 39pp; English.
XX AAT47264-T47280 represent capped RNA molecules produced by the method of
CC the invention. The method of the invention is for producing capped RNA
CC or RNA analogues. The method comprises reacting a RNA or analogue
CC oligonucleotide with a phosphate addition agent to form a RNA or
CC analogue mono-, di- or triphosphate, which is then capped. The presence
CC of the cap is important for mRNA maturation, initiation of translation,
CC and protects the mRNA against various RNases present in the cell. The
CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
CC treating or preventing an influenza infection in an animal. The synthetic
CC capped RNA are substrates for virally encoded endonuclease associated
CC with influenza virus. The short non-extendible (due to their length or
CC because of the modification of the 3' end of the oligo) RNA molecules are
CC potent inhibitors of the cleavage of capped RNA by influenza
CC endonuclease. They may be used to investigate viral and cellular
CC mechanisms of transcription/translation, or mRNA maturation.
XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
SQ Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Qy 1521 TTTATATTTTAACTTT 1537
Db 2 UUUUUUUUUUUUUUUU 18

RESULT 217
AAT47271
ID AAT47271 standard; RNA; 19 BP.
XX AC AAT47271;
XX DT 28-AUG-1997 (first entry)
XX DE Capped RNA influenza endonuclease substrate #5.
XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= triphosphorylated
FT modified_base 2 /*tag= b
FT /*mod_base= 2'-O-methyluridine
FT modified_base 6 /*tag= c
FT /*mod_base= 2'-deoxy-2'-fluoro-uridine
FT modified_base 12 /*tag= d
FT /*mod_base= 2'-deoxy-2'-fluoro-uridine
XX MO9640159-A1.
XX 19-DEC-1996.
XX

PR 07-JUN-1995; 95US-0480068.
XX (MERI ) MERCK & CO INC.
XX Benseler F, Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-051868/05.
XX Production of capped RNA or analogues - useful as substrates for
FT Influenza virus associated virally encoded endonuclease
XX Claim 18; Page 13; 39pp; English.
XX AAT47264-T47280 represent capped RNA molecules produced by the method of
CC the invention. The method of the invention is for producing capped RNA
CC or RNA analogues. The method comprises reacting a RNA or analogue
CC oligonucleotide with a phosphate addition agent to form a RNA or
CC analogue mono-, di- or triphosphate, which is then capped. The presence
CC of the cap is important for mRNA maturation, initiation of translation,
CC and protects the mRNA against various RNases present in the cell. The
CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
CC treating or preventing an influenza infection in an animal. The synthetic
CC capped RNA are substrates for virally encoded endonuclease associated
CC with influenza virus. The short non-extendible (due to their length or
CC because of the modification of the 3' end of the oligo) RNA molecules are
CC potent inhibitors of the cleavage of capped RNA by influenza
CC endonuclease. They may be used to investigate viral and cellular
CC mechanisms of transcription/translation, or mRNA maturation.
XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
SQ Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Qy 1521 TTTATATTTTAACTTT 1537
Db 2 UUUUUUUUUUUUUUUU 18

RESULT 218
AAT47272
ID AAT47272 standard; RNA; 19 BP.
XX AC AAT47272;
XX DT 28-AUG-1997 (first entry)
XX DE Capped RNA influenza endonuclease substrate #6.
XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= triphosphorylated
FT modified_base 2 /*tag= b
FT /*mod_base= 2'-O-methyluridine
FT modified_base 6 /*tag= c
FT /*mod_base= 2'-deoxy-2'-fluoro-uridine
FT modified_base 12 /*tag= d
FT /*mod_base= 2'-deoxy-2'-fluoro-uridine
FT modified_base 13 /*tag= e
FT /*mod_base= 2'-deoxy-2'-fluoro-adenosine

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XX PN WO9640159-A1.
XX PD 19-DEC-1996.
XX PF 03-JUN-1996; 96WO-US08394.
XX PR 07-JUN-1995; 95US-0480068.
XX PA (MERI ) MERCK & CO INC.
XX PI Benseler F, Cole JL, Kuo LC, Olsen DB;
XX DR WPI; 1997-051868/05.
XX PT Production of capped RNA or analogues - useful as substrates for
XX PT influenza virus associated virally encoded endonuclease
XX PS Claim 18; Page 14; 39pp; English.
XX CC AAT47264-T47280 represent capped RNA molecules produced by the method of
XX CC the invention. The method of the invention is for producing capped RNA
XX CC or RNA analogues. The method comprises reacting a RNA or analogue
XX CC oligonucleotide with a phosphate addition agent to form a RNA or
XX CC analogue mono-, di- or triphosphate, which is then capped. The presence
XX CC of the cap is important for mRNA maturation, initiation of translation,
XX CC and protects the mRNA against various RNases present in the cell. The
XX CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
XX CC treating or preventing an influenza infection in an animal. The synthetic
XX CC capped RNA are substrates for virally encoded endonuclease associated
XX CC with influenza virus. The short non-extendible (due to their length or
XX CC because of the modification of the 3' end of the oligo) RNA molecules are
XX CC potent inhibitors of the cleavage of capped RNA by influenza
XX CC endonuclease. They may be used to investigate viral and cellular
XX CC mechanisms of transcription/translation, or mRNA maturation.
XX SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537
DB 2 UUUUUUUUUUUUUUUU 18

RESULT 219
AAT47273
ID AAT47273 standard; RNA; 19 BP.
AC AAT47273;
DT 28-AUG-1997 (first entry)
DE Capped RNA influenza endonuclease substrate #7.
XX Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*mod_base= triphosphorylated
XX modified_base 2 /*tag= b
XX /*mod_base= 2'-O-methyluridine
XX misc_feature 19 /*tag= c
XX /*note= "biotin labelled for attachment to solid support"
XX PD 19-DEC-1996.
XX XX
```

```
PN WO9640159-A1.
PD 19-DEC-1996.
PF 03-JUN-1996; 96WO-US08394.
PR 07-JUN-1995; 95US-0480068.
PA (MERI ) MERCK & CO INC.
PI Benseler F, Cole JL, Kuo LC, Olsen DB;
DR WPI; 1997-051868/05.
PT Production of capped RNA or analogues - useful as substrates for
PT influenza virus associated virally encoded endonuclease
PS Claim 18; Page 14; 39pp; English.
CC AAT47264-T47280 represent capped RNA molecules produced by the method of
CC the invention. The method of the invention is for producing capped RNA
CC or RNA analogues. The method comprises reacting a RNA or analogue
CC oligonucleotide with a phosphate addition agent to form a RNA or
CC analogue mono-, di- or triphosphate, which is then capped. The presence
CC of the cap is important for mRNA maturation, initiation of translation,
CC and protects the mRNA against various RNases present in the cell. The
CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
CC treating or preventing an influenza infection in an animal. The synthetic
CC capped RNA are substrates for virally encoded endonuclease associated
CC with influenza virus. The short non-extendible (due to their length or
CC because of the modification of the 3' end of the oligo) RNA molecules are
CC potent inhibitors of the cleavage of capped RNA by influenza
CC endonuclease. They may be used to investigate viral and cellular
CC mechanisms of transcription/translation, or mRNA maturation.
SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 3e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537
DB 2 UUUUUUUUUUUUUUUU 18

RESULT 220
AAT47267
ID AAT47267 standard; RNA; 19 BP.
AC AAT47267;
DT 28-AUG-1997 (first entry)
DE Capped RNA influenza endonuclease substrate #1.
XX Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*mod_base= triphosphorylated
XX modified_base 2 /*tag= b
XX /*mod_base= 2'-O-methyluridine
XX PN WO9640159-A1.
XX PD 19-DEC-1996.
XX XX
```


PT influenza virus associated virally encoded endonuclease

PS Claim 18; Page 14; 39pp; English.

XX AAT47264-T47280 represent capped RNA molecules produced by the method of
 CC the invention. The method of the invention is for producing capped RNA
 CC or RNA analogues. The method comprises reacting a RNA or analogue
 CC oligonucleotide with a phosphate addition agent to form a RNA or
 CC analogue mono-, di- or triphosphate, which is then capped. The presence
 CC of the cap is important for mRNA maturation, initiation of translation,
 CC and protects the mRNA against various RNases present in the cell. The
 CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
 CC treating or preventing an influenza infection in an animal. The synthetic
 CC capped RNA are substrates for virally encoded endonuclease associated
 CC with influenza virus. The short non-extendible (due to their length or
 CC because of the modification of the 3' end of the oligo) RNA molecules are
 CC potent inhibitors of the cleavage of capped RNA by influenza
 CC endonuclease. They may be used to investigate viral and cellular
 CC mechanisms of transcription/translation, or mRNA maturation.

XX SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 17.6%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;

Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537

DB 2 UUUUUUUUUUUUUU 18

RESULT 223

AAT47277

ID AAT47277 standard; RNA; 19 BP.

XX AC AAT47277;

XX DT 28-AUG-1997 (first entry)

XX DE Capped RNA influenza endonuclease substrate #9.

XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
 KW endonuclease aptamer; RNase; therapy; inhibitor; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1 /tag= a

FT /mod_base= triphosphorylated

FT modified_base 2 /tag= b

FT /mod_base= 2'-O-methyluridine

FT modified_base 3 /tag= c

FT /mod_base= 2'-O-methyluridine

XX PN WO9640159-A1.

XX PD 19-DEC-1996.

XX PF 03-JUN-1996; 96WO-US08394.

XX PR 07-JUN-1995; 95US-0480068.

XX PA (MERI) MERCK & CO INC.

XX PI Benseler F, Cole JL, Kuo LC, Olsen DB;

XX DR WPI; 1997-051868/05.

XX XX Production of capped RNA or analogues - useful as substrates for
 PT influenza virus associated virally encoded endonuclease

XX Claim 18; Page 15; 39pp; English.

XX AAT47264-T47280 represent capped RNA molecules produced by the method of
 CC the invention. The method of the invention is for producing capped RNA
 CC or RNA analogues. The method comprises reacting a RNA or analogue
 CC oligonucleotide with a phosphate addition agent to form a RNA or
 CC analogue mono-, di- or triphosphate, which is then capped. The presence
 CC of the cap is important for mRNA maturation, initiation of translation,
 CC and protects the mRNA against various RNases present in the cell. The
 CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
 CC treating or preventing an influenza infection in an animal. The synthetic
 CC capped RNA are substrates for virally encoded endonuclease associated
 CC with influenza virus. The short non-extendible (due to their length or
 CC because of the modification of the 3' end of the oligo) RNA molecules are
 CC potent inhibitors of the cleavage of capped RNA by influenza
 CC endonuclease. They may be used to investigate viral and cellular
 CC mechanisms of transcription/translation, or mRNA maturation.

XX SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 17.6%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;

Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537

DB 2 UUUUUUUUUUUUUU 18

RESULT 224

AAT47278

ID AAT47278 standard; RNA; 19 BP.

XX AC AAT47278;

XX DT 28-AUG-1997 (first entry)

XX DE Capped RNA influenza endonuclease substrate #10.

XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
 KW endonuclease aptamer; RNase; therapy; inhibitor; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1 /tag= a

FT /mod_base= triphosphorylated

FT modified_base 2 /tag= b

FT /mod_base= 2'-O-methyluridine

FT modified_base 13 /tag= c

FT /mod_base= phosphorothioated

XX PN WO9640159-A1.

XX PD 19-DEC-1996.

XX PF 03-JUN-1996; 96WO-US08394.

XX PR 07-JUN-1995; 95US-0480068.

XX PA (MERI) MERCK & CO INC.

XX PI Benseler F, Cole JL, Kuo LC, Olsen DB;

XX DR WPI; 1997-051868/05.

XX XX Production of capped RNA or analogues - useful as substrates for
 PT influenza virus associated virally encoded endonuclease

PS Claim 18; Page 15; 39pp; English.

XX AAT47264-T47280 represent capped RNA molecules produced by the method of

CC the invention. The method of the invention is for producing capped RNA

CC or RNA analogues. The method comprises reacting a RNA or analogue

CC oligonucleotide with a phosphate addition agent to form a RNA or

CC analogue mono-, di- or triphosphate, which is then capped. The presence

CC of the cap is important for mRNA maturation, initiation of translation,

CC and protects the mRNA against various RNases present in the cell. The

CC capped RNA or analogue is an influenza endonuclease aptamer, useful for

CC treating or preventing an influenza infection in an animal. The synthetic

CC capped RNA are substrates for virally encoded endonuclease associated

CC with influenza virus. The short non-extendible (due to their length or

CC because of the modification of the 3' end of the oligo) RNA molecules are

CC potent inhibitors of the cleavage of capped RNA by influenza

CC endonuclease. They may be used to investigate viral and cellular

CC mechanisms of transcription/translation, or mRNA maturation.

XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

SQ

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 17.6%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;

Matches 3; Conservative 12; Mismatches 2;

QY 1521 TTTATATTTTAACTTT 1537

Db 2 UUUUUUUUUUUUUUUU 18

RESULT 225

AAT47279

ID AAT47279 standard; RNA; 19 BP.

AC AAT47279;

DT 28-AUG-1997 (first entry)

DE Capped RNA influenza endonuclease substrate #11.

KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;

KW endonuclease aptamer; RNase; therapy; inhibitor; ss.

OS Synthetic.

PH Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT /*mod_base= triphosphorylated

FT modified_base 2 /*tag= b

FT /*mod_base= 2'-O-methyluridine

FT modified_base 12 /*tag= c

FT /*mod_base= phosphorothioated

FT modified_base 13 /*tag= d

FT /*mod_base= phosphorothioated

FT modified_base 14 /*tag= e

FT /*mod_base= phosphorothioated

XX W09640159-A1.

XX 19-DEC-1996.

XX 03-JUN-1996; 96WO-US08394.

XX 07-JUN-1995; 95US-0480068.

XX (MERI) MERCK & CO INC.

XX Benseiler F, Cole JL, Kuo LC, Olsen DB;

DR WPI; 1997-051868/05.

XX Production of capped RNA or analogues - useful as substrates for

PT influenza virus associated virally encoded endonuclease

XX Claim 18; Page 15; 39pp; English.

XX AAT47264-T47280 represent capped RNA molecules produced by the method of

CC the invention. The method of the invention is for producing capped RNA

CC or RNA analogues. The method comprises reacting a RNA or analogue

CC oligonucleotide with a phosphate addition agent to form a RNA or

CC analogue mono-, di- or triphosphate, which is then capped. The presence

CC of the cap is important for mRNA maturation, initiation of translation,

CC and protects the mRNA against various RNases present in the cell. The

CC capped RNA or analogue is an influenza endonuclease aptamer, useful for

CC treating or preventing an influenza infection in an animal. The synthetic

CC capped RNA are substrates for virally encoded endonuclease associated

CC with influenza virus. The short non-extendible (due to their length or

CC because of the modification of the 3' end of the oligo) RNA molecules are

CC potent inhibitors of the cleavage of capped RNA by influenza

CC endonuclease. They may be used to investigate viral and cellular

CC mechanisms of transcription/translation, or mRNA maturation.

XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

SQ

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 17.6%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;

Matches 3; Conservative 12; Mismatches 2;

QY 1521 TTTATATTTTAACTTT 1537

Db 2 UUUUUUUUUUUUUUUU 18

RESULT 226

AAV49123

ID AAV49123 standard; DNA; 19 BP.

AC AAV49123;

XX AAV49123;

DT 15-OCT-1998 (first entry)

DE rb gene antisense oligonucleotide rb-N-71.

XX rb gene; antisense oligonucleotide; modulate; gene expression; ss.

XX Synthetic.

OS Homo sapiens.

XX EP856579-A1.

XX 05-AUG-1998.

XX 31-JAN-1997; 97EP-0101531.

XX 31-JAN-1997; 97EP-0101531.

XX (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.

XX Brysch W, Schlingensiepen K;

XX WPI; 1998-400910/35.

XX Preparation of antisense oligonucleotide(s) which lack long runs of

PT consecutive guanosine or inosine - and have specific ratio of

PT residues able to form two or three hydrogen bonds, have greater

PT activity and reduced toxicity, used therapeutically or to modulate

PT growth of cells in culture

XX Example 7; Fig 9b; 286pp; English.

XX AAV49008-236 represent antisense oligonucleotides directed against

CC the rb gene. Of these, only oligonucleotides AAV49008-52 resulted in

CC effective downregulation of negative growth control by rb, while
 CC oligonucleotides AAV49052-236 had little effect. The oligonucleotides
 CC exemplify the invention. The specification describes oligonucleotides
 CC that contain 8-30 nucleotides, which contain at most 8 nucleotides
 CC that can each form three hydrogen bonds to cytosine; do not contain
 CC four consecutive nucleotides able to form three H-bonds each to four
 CC consecutive cytosines; do not contain two sequences of three consecutive
 CC nucleotides each able to form three H-bonds to form two H-bonds
 CC each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
 CC oligonucleotides are used to modulate expression of genes, particularly
 CC the genes for p53, Erb-2, junB, junD, TGF-beta 1 or beta 2 to control
 CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
 CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
 CC oligonucleotides can also be used to analyse function of proteins (by
 CC altering their expression or activity) and therapeutically, e.g. in
 CC cases of cancer or (targeting TGF) for stimulating the immune system.
 CC
 XX Sequence 19 BP; 6 A; 1 C; 1 G; 11 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. NO. 3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 TTTATTAGATAAATTTC 1188
 ||||| ||||| ||||| |||||
 Db 1 TTTTAAAGTAATTTC 17

RESULT 227
 AAV26328
 ID AAV26328 standard; DNA; 19 BP.
 XX
 AC AAV26328;
 XX
 DT 07-AUG-1998 (first entry)
 XX
 DE Human prostate cancer marker UC Band #201 identifying RT-PCR primer 1.
 XX
 KW Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.

OS Synthetic.
 OS Homo sapiens.
 XX WO9804689-A1.
 XX 05-FEB-1998.
 XX 31-JUL-1996; 96WO-US12516.
 XX 31-JUL-1996; 96WO-US12516.
 XX (UROC-) UROC INC.
 XX An G, O'hara SM, Ralph D, Veltri R;
 XX WPI; 1998-130681/12.
 DR Human prostate cancer marker - useful for detection and treatment of
 PT human prostate cancer
 PT
 XX Example 4; Page 120; 229pp; English.

XX This primer is used in the relative quantitative RT-PCR to examine the
 CC expression of the genes which is used for the identification of markers
 CC of human prostate cancer. Isolated nucleic acid segments shown in
 CC AAV16881 to AAV16885, AAV16890 to AAV16903, AAV26351 and AAV26352 which
 CC can act as human prostate cancer markers are provided in the
 CC specification. The specification also provides methods for identifying
 CC markers for human prostate cancer and for detection of prostate cancer
 CC cells. The markers can be identified by amplifying human prostate RNA to
 CC provide nucleic acid amplification products, separating the products and
 CC identifying those RNA that are differentially expressed between human

CC prostate cancers versus normal or benign human prostate. Prostate cancer
 CC cells in a sample can be detected by detecting a nucleic acid in a
 CC sample, the nucleic acid being a prostate cancer marker. Primers and
 CC probes derived from this marker can be used for the detection of prostate
 CC cancer cells in a sample. Antibodies against the protein encoded by the
 CC marker nucleic acid fragments, inhibitors of the protein and
 CC oligonucleotides antisense to the markers can be used in the treatment of
 CC prostate cancer. The antibodies can also be used for the diagnosis of
 CC human prostate cancer.

XX Sequence 19 BP; 9 A; 2 C; 4 G; 4 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. NO. 3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1211 AAACAAACAATTGGGTA 1227
 ||||| ||||| ||||| |||||
 Db 1 AAACAAACGTTTGGGTA 17

RESULT 228
 AAZ74461
 ID AAZ74461 standard; DNA; 19 BP.
 XX
 AC AAZ74461;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human biallelic marker downstream amplification primer SEQ ID NO:8917.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

OS Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB00822.

XX 21-APR-1998; 98US-0082614.

XX 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome -

PS Claim 8; Page 2110; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses; they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.

XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.

SQ Sequence 19 BP; 11 A; 6 C; 1 G; 1 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1208 AACCAACAAACAATGG 1224

Db 1 AACCAACAAACAATAG 17

RESULT 229

AAH58843
 ID AAH58843 standard; DNA; 19 BP.

XX

AC AAH58843;

DT 04-DEC-2000 (first entry)

DE cdk-we-hu ribozyme binding site #156.

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;

KW restenosis; ss.

XX

OS Mammalia.

PN WO200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US28772.

PR 04-DEC-1998; 98US-0110954.

PA (IMMU-) IMMUSOL INC.

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -

XX Disclosure; Page 65; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAH58843 to AAH58843. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.

XX Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1378 TACGGAATATGAGTTA 1394

Db 2 TACGGAATATGAGTTA 18

RESULT 230

AAH58843

ID AAH58843 standard; DNA; 19 BP.

XX

AC AAH58843;

DT 10-SEP-2001 (first entry)

DE cdk-we-hu ribozyme binding site SEQ ID NO:1267.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; WMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiskinning; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.

XX Homo sapiens.

OS Synthetic.

PN WO200130362-A2.

PD 03-MAY-2001.

PF 26-OCT-2000; 2000WO-US29500.

PR 26-OCT-1999; 99US-0161532.

PA (IMMU-) IMMUSOL INC.

PI Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -

XX Example 1; Page 164; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskinning,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH58843 to AAH58843 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1378 TACGGAATATGAGTTA 1394

Db 2 TACGGAATATGAGTTA 18

RESULT 231

```

ABZ01793/c
ID ABZ01793 standard; DNA; 50 BP.
XX
AC ABZ01793;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 1784.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US47856.
XX
PF 20-OCT-2000; 2000US-241994P.
XX
PR 08-JUN-2001; 2001US-296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides
XX
XX Claim 1; Page 382; 2038pp; English.
XX
XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
XX
SQ Sequence 50 BP; 17 A; 8 C; 13 G; 12 T; 0 other;

Query Match 1.1%; Score 13.8; DB 1; Length 50;
Best Local Similarity 58.5%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 703 CCAAGAGATATCCGAACTTAAATTTTACGGAATTTGAATGG 743
DB 49 CCCATTCAATCTCTGAAATTAAGTTCCGATATCTCTGG 9

RESULT 232
AAD26678/c
ID AAD26678 standard; DNA; 15 BP.
XX
AC AAD26678;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human GPR31 gene polymorphism detecting ASO primer #1.
XX
XX Human; G-protein coupled receptor 31; GPR31 protein; haplotyping;

```

```

KW genotyping; gene therapy; cancer; polymorphism; ASO; primer;
KW allele-specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200190124-A2.
XX
PD 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US16908.
XX
XX 23-MAY-2000; 2000US-206572P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bieglecki KM, Duda A, Kazemi A, Lee HH, Messer C;
XX WPI; 2002-089915/12.
XX
XX Novel genetic variants of G-protein coupled receptor gene useful in
PT studying expression and function of the protein, and for screening
PT drugs to treat diseases e.g. cancer
XX
XX Claim 16; Page 13; 75pp; English.
XX
XX The invention relates to genetic variants of human G-protein coupled
CC receptor 31 (GPR31) gene. The invention also relates to compositions
CC and methods for haplotyping and/or genotyping the GPR31 gene in an
CC individual. Polynucleotides of the invention are useful in studying
CC the expression and function of GPR31, and in expressing GPR31 protein
CC for use in screening candidate drugs to treat diseases related to
CC GPR31 activity and in studying the effect of the variation on the
CC biological activity of GPR31 as well as on the binding affinity of
CC candidate drugs targeting GPR31 for the treatment of cancer. They
CC are also used in gene therapy. The haplotyping method is useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated
CC with GPR31 activity e.g. cancer. This method is also useful for
CC haplotyping GPR31 gene in an individual, which can also be used by
CC the pharmaceutical research scientist to validate GPR31 as a candidate
CC target for, and in design of clinical trials of candidate drugs, for
CC treating a specific condition drugs or disease predicted to be
CC associated with GPR31 activity. The present sequence is an allele
CC specific oligonucleotide (ASO) primer used to detect human GPR31
CC gene polymorphisms.
XX
SQ Sequence 15 BP; 10 A; 0 C; 1 G; 3 T; 1 other;

Query Match 1.1%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1142 ATTTATTTTATTTT 1155
DB 15 AWTATTTTATTTT 2

RESULT 233
ABQ79871
ID ABQ79871 standard; DNA; 20 BP.
XX
XX ABQ79871;
XX
XX 23-DEC-2002 (first entry)
XX
XX Nucleotide sequence of a PCR primer #1.
XX
XX Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
XX Synthetic.
XX
XX JP2002191369-A.

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XX PD 09-JUL-2002.
XX PF 27-DEC-2000; 2000JP-0399573.
XX PR 27-DEC-2000; 2000JP-0399573.
XX PA (TOJO ) TOYO KOHAN CO LTD.
XX PA (TAKA/) TAKAHASHI K.
XX DR WPI; 2002-630904/68.
XX PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by
XX PT using a substrate on which a DNA is immobilized used in medical,
XX PT biochemical, molecular biological and gene engineering fields -
XX PS Examples; Page 9; 13pp; Japanese.
XX CC The invention relates to performing a thermal cycle of PCR by using a
XX CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
XX CC method is useful in the medical, biochemical, molecular biological and
XX CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
XX CC used in the method of the invention.
XX SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
      Query Match      1.1%; Score 13.6; DB 1; Length 20;
      Best Local Similarity 80.0%; Pred. No. 3.5e+02;
      Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1560 AAATTTTTTCTGTTCT 1579
Db 1 AAATTTTTTCTGTTCT 20

RESULT 234
AAQ64706
ID AAQ64706 standard; cDNA to mRNA; 22 BP.
XX AC AAQ64706;
XX DT 25-MAR-2003 (updated)
XX DT 04-JAN-1995 (first entry)
XX DE 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX KW antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
XX KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 1..4
XX FT /*tag= a
XX FT /label= 2',5'-linked tetraadenylate
XX FT /note= "nucleotides linked through phosphodiester
XX FT bonds at hydroxyl groups of 2' and 5'
XX FT carbons"
XX FT misc_feature 5..22
XX FT /*tag= b
XX FT /note= "antisense region"
XX PN WO9409129-A2.
XX PD 28-APR-1994.
XX XX 20-OCT-1993; 93WO-US10103.
XX XX 21-OCT-1992; 92US-0965666.
XX PR 17-SEP-1993; 93US-0123449.
XX PA (CLEV-) CLEVELAND CLINTC RES INST.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

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XX PI Lesiak K, Maitra R, Silverman R, Torrence P;
XX DR WPI; 1994-151315/18.
XX PT Specific cleavage of RNA, useful partic. for treating viral
XX PT infection, cancers, etc. - by using anti-sense oligonucleotide
XX PT coupled to activator of 2-5A dependent RNase
XX PS Example 1; Page 68; 86pp; English.
XX CC This sequence is an example of a 2-5A-antisense oligonucleotide
XX CC chimeric molecule. The antisense region targets the chimeric
XX CC molecule to a particular region of RNA to be specifically
XX CC cleaved and the 2',5'-linked tetraadenylate tail activates
XX CC the 2-5A RNase. Typical applications are treatment of viral
XX CC infections (esp. for cleavage of an RNA virus genome), cancer;
XX CC leukaemia, cardiovascular disorders (e.g. restenosis after
XX CC angioplasty), genetic disorders, osteoarthritis or rheumatoid
XX CC arthritis.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 other;
      Query Match      1.1%; Score 13.6; DB 1; Length 22;
      Best Local Similarity 80.0%; Pred. No. 3.8e+02;
      Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1560 AAATTTTTTCTGTTCT 1579
Db 2 AAATTTTTTCTGTTCT 21

RESULT 235
AAL55126
ID AAL55126 standard; DNA; 30 BP.
XX AC AAL55126;
XX DT 16-APR-2003 (first entry)
XX DE Nucleic acid synthesising method related PCR primer, SEQ ID No 7.
XX KW Synthesising; target base sequence; annealing; genetic disease; SNP;
XX KW single nucleotide polymorphism; cancer; PCR; primer; ss.
XX OS Unidentified.
XX PN WO200290538-A1.
XX PD 14-NOV-2002.
XX PF 08-MAY-2002; 2002WO-JP04479.
XX PR 08-MAY-2001; 2001JP-0137060.
XX PR 18-JUN-2001; 2001JP-0184131.
XX PA (SIKE ) EIKEN KAGAKU KK.
XX PI Nagamine K;
XX XX WPI; 2003-120547/11.
XX PT Synthesizing target base sequence-containing nucleic acids constituting
XX PT complementary base sequences against template by the LAMP method,
XX PT applicable in identifying genetic diseases, cancerization and
XX PT microorganisms -
XX PS Example 1; Page 62; 107pp; Japanese.
XX CC The invention relates to a novel method for synthesising a target base
XX CC sequence-containing nucleic acids. The method comprises the formation of
XX CC single-stranded nucleic acids; synthesis of complementary strand by

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CC annealing; and producing single-stranded nucleic acid from a target base
 CC sequence by the synthesis of a complementary strand by annealing of a
 CC complementary base sequence. The method is useful for synthesizing a
 CC target base sequence-containing nucleic acids, which is applicable in
 CC detecting SNP (single nucleotide polymorphism) in genes, identifying
 CC genetic diseases, cancer and microorganisms. Such a method can be
 CC easily, rapidly and freely carried out without being influenced by
 CC contamination or complicated temperature control, but with improved
 CC reaction specificity, high accuracy and efficiency, operable at low cost.
 CC This polynucleotide sequence represents a PCR primer used in the
 CC synthesizing method of the invention.

SQ Sequence 30 BP; 15 A; 2 C; 2 G; 11 T; 0 other;
 Query Match 1.1%; Score 13.6; DB 1; Length 30;
 Best Local Similarity 57.3%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 9;

QY 753 ATGTGATATTGAAGCATCACAATAAAA 780
 DB 3 ATTGTGCTTAATAATACATAATA 30

RESULT 236
 AAT56350
 ID AAT56350 standard; RNA; 15 BP.

AC AAT56350;

DT 25-MAR-2003 (updated)
 DT 14-MAY-1997 (first entry)

XX Mouse TNF-a hammerhead ribozyme target sequence (nt position 1326).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

XX Mus musculus.

XX OS

XX PN

XX PD

XX PF

XX PP

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Ueman N, Wincott PE, Woolf T;
 PI WPI; 1995-351090/45.

XX Ribozyms having modified bases and methods for producing them -

XX for use in inhibiting disease related genes

XX Claim 2; Page 252; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.

CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;

SQ Query Match 1.1%; Score 13.4; DB 1; Length 15;

XX Best Local Similarity 26.7%; Pred. No. 2.9e+02;

XX Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1043 ATTATTATGATTT 1057

DB 1 AUAUUUUUUUUUU 15

XX RESULT 237

XX AAT56326

XX ID AAT56326 standard; RNA; 15 BP.

XX AC AAT56326;

XX DT 25-MAR-2003 (updated)

XX DT 14-MAY-1997 (first entry)

XX DE Mouse TNF-a hammerhead ribozyme target sequence (nt position 1311).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

XX Mus musculus.

XX OS

XX PN

XX PD

XX PF

XX PR 30-JAN-1995; 95WO-IB00156.
 XX PR 23-FEB-1994; 94US-0201109.
 XX PR 29-MAR-1994; 94US-0218934.
 XX PR 04-APR-1994; 94US-0222795.
 XX PR 07-APR-1994; 94US-0224483.
 XX PR 15-APR-1994; 94US-0227958.
 XX PR 15-APR-1994; 94US-0228041.
 XX PR 18-MAY-1994; 94US-0245736.
 XX PR 06-JUL-1994; 94US-0271280.
 XX PR 15-AUG-1994; 94US-0291932.
 XX PR 16-AUG-1994; 94US-0291433.
 XX PR 17-AUG-1994; 94US-0292620.
 XX PR 19-AUG-1994; 94US-0293520.
 XX PR 02-SEP-1994; 94US-0300000.
 XX PR 08-SEP-1994; 94US-0303039.
 XX PR 23-SEP-1994; 94US-0311486.
 XX PR 23-SEP-1994; 94US-0311749.
 XX PR 28-SEP-1994; 94US-0314397.
 XX PR 03-OCT-1994; 94US-0316771.

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PN W09523225-A2.
XX 31-AUG-1995.
XX 23-FEB-1995; 95WO-IB00155.
XX 30-JAN-1995; 95US-0380734.
PR 23-FEB-1994; 94US-0201109.
PR 29-MAR-1994; 94US-0218934.
PR 04-APR-1994; 94US-0223795.
PR 07-APR-1994; 94US-0224483.
PR 15-APR-1994; 94US-0227958.
PR 15-APR-1994; 94US-0228041.
PR 18-MAY-1994; 94US-0245736.
PR 06-JUL-1994; 94US-0271280.
PR 15-AUG-1994; 94US-0291932.
PR 16-AUG-1994; 94US-0291433.
PR 17-AUG-1994; 94US-0292620.
PR 19-AUG-1994; 94US-0293520.
PR 02-SEP-1994; 94US-0300000.
PR 08-SEP-1994; 94US-0303039.
PR 23-SEP-1994; 94US-0311486.
PR 23-SEP-1994; 94US-0311749.
PR 28-SEP-1994; 94US-0314397.
PR 03-OCT-1994; 94US-0316771.
PR 07-OCT-1994; 94US-0319492.
PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LM;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them -
PT for use in inhibiting disease related genes
XX Claim 2; Page 252; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
SQ
Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
Qy 1039 ATTATTATTATAT 1053
Db 1 AUUUUUUUUUUUU 15

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RESULT 238
AAT56332
ID AAT56332 standard; RNA; 15 BP.
XX
XX AAT56332;
AC
XX
XX 25-MAR-2003 (updated)
DT 14-MAY-1997 (first entry)
XX
XX Mouse TNF-a hammerhead ribozyme target sequence (nt position 1313).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome;
XX AIDS; ss.
XX
XX Mus musculus.
OS
XX
XX W09523225-A2.
PN
XX
XX 31-AUG-1995.
PD
XX
XX 23-FEB-1995; 95WO-IB00156.
XX
XX 30-JAN-1995; 95US-0380734.
PR 23-FEB-1994; 94US-0201109.
PR 29-MAR-1994; 94US-0218934.
PR 04-APR-1994; 94US-0223795.
PR 07-APR-1994; 94US-0224483.
PR 15-APR-1994; 94US-0227958.
PR 15-APR-1994; 94US-0228041.
PR 18-MAY-1994; 94US-0245736.
PR 06-JUL-1994; 94US-0271280.
PR 15-AUG-1994; 94US-0291932.
PR 16-AUG-1994; 94US-0291433.
PR 17-AUG-1994; 94US-0292620.
PR 19-AUG-1994; 94US-0293520.
PR 02-SEP-1994; 94US-0300000.
PR 08-SEP-1994; 94US-0303039.
PR 23-SEP-1994; 94US-0311486.
PR 23-SEP-1994; 94US-0311749.
PR 28-SEP-1994; 94US-0314397.
PR 03-OCT-1994; 94US-0316771.
PR 07-OCT-1994; 94US-0319492.
PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LM;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them -
PT for use in inhibiting disease related genes
XX Claim 2; Page 252; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC

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CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 26.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 QY 1041 TTATTATTATGTAT 1055
 Db 1 UUAUUAUUUAUUU 15
 RESULT 239
 AAT56338
 ID AAT56338 standard; RNA; 15 BP.
 XX
 AC AAT56338;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-MAY-1997 (first entry)
 XX
 DE Mouse TNF-a hammerhead ribozyme target sequence (nt position 1314).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 QS Mus musculus.
 XX
 DN W09523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.

PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowirza B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-adamic J, McSwiggan JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Ueman N, Wincott PE, Woolf T;
 XX
 DR WPI; 1995-351090/45.
 XX
 PT Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 252; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 26.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 QY 1042 TTATTATTATGTAT 1056
 Db 1 UUAUUAUUUAUUU 15
 RESULT 240
 AAT55813
 ID AAT55813 standard; RNA; 15 BP.
 XX
 AC AAT55813;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human TNF-alpha hammerhead ribozyme target sequence (nt position 1270).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

OS Homo sapiens.
 XX WO9523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB00156.
 XX 30-JAN-1995; 95US-0380734.
 XX 21-FEB-1994; 94US-0201109.
 XX 29-MAR-1994; 94US-0218934.
 XX 04-APR-1994; 94US-0222795.
 XX 07-APR-1994; 94US-0224483.
 XX 15-APR-1994; 94US-0227958.
 XX 18-MAY-1994; 94US-0228041.
 XX 06-JUL-1994; 94US-0271280.
 XX 15-AUG-1994; 94US-0291932.
 XX 16-AUG-1994; 94US-0291433.
 XX 17-AUG-1994; 94US-0292620.
 XX 19-AUG-1994; 94US-0293520.
 XX 02-SEP-1994; 94US-0300000.
 XX 08-SEP-1994; 94US-0303039.
 XX 23-SEP-1994; 94US-0311486.
 XX 28-SEP-1994; 94US-0314397.
 XX 03-OCT-1994; 94US-0316771.
 XX 07-OCT-1994; 94US-0319492.
 XX 11-OCT-1994; 94US-0321993.
 XX 04-NOV-1994; 94US-0334847.
 XX 10-NOV-1994; 94US-0337608.
 XX 28-NOV-1994; 94US-0345516.
 XX 16-DEC-1994; 94US-0357577.
 XX 23-DEC-1994; 94US-0363233.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 XX Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 XX Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozymes having modified bases and methods for producing them -
 XX for use in inhibiting disease related genes
 XX Claim 2; Page 243; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 XX mRNA at the nucleotide base position indicated in the DE line.
 XX Regions of the mRNA that do not form secondary folding
 XX structures and that contain potential hammerhead and hairpin
 XX ribozyme cleavage sites were identified by computer analysis.
 XX Ribozymes directed against these mRNA sequences were designed and
 XX synthesised with modifications that improve their nuclease
 XX resistance. The ribozymes are designed to cleave the target
 XX sequences and thereby inhibit TNF-alpha expression, making them
 XX potentially useful for treating rheumatoid arthritis, septic shock
 XX and other inflammatory disorders including psoriasis, as well as
 XX for treatment of AIDS.
 XX (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
 XX Query Match 1.1%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 26.7%; Pred. No. 2.9e+07;
 XX Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 Qy 1039 ATTATTATTATCT 1053
 Db 1 AUUUUUUUUUUU 15

RESULT 241
 AAT55815
 ID AAT55815 standard; RNA; 15 BP.
 XX AC
 XX AAT55815;
 XX DT
 XX 25-MAR-2003 (updated)
 XX DT
 XX 25-MAR-1997 (first entry)
 XX DE
 XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1272).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 XX intercellular adhesion molecule; rel A; tumour necrosis factor;
 XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 XX translocation; chronic myelogenous leukaemia; CML; cancer;
 XX Philadelphia chromosome; inflammation; autoimmune disease;
 XX atherosclerosis; myocardial infarction; stroke; restenosis;
 XX transplant rejection; rheumatoid arthritis; psoriasis;
 XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 XX human immunodeficiency virus; acquired immune deficiency syndrome;
 XX AIDS; ss.
 XX OS
 XX Homo sapiens.
 XX WO9523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB00156.
 XX 30-JAN-1995; 95US-0380734.
 XX 23-FEB-1994; 94US-0201109.
 XX 29-MAR-1994; 94US-0218934.
 XX 04-APR-1994; 94US-0222795.
 XX 07-APR-1994; 94US-0224483.
 XX 15-APR-1994; 94US-0227958.
 XX 18-MAY-1994; 94US-0228041.
 XX 06-JUL-1994; 94US-0271280.
 XX 15-AUG-1994; 94US-0291932.
 XX 16-AUG-1994; 94US-0291433.
 XX 17-AUG-1994; 94US-0292620.
 XX 19-AUG-1994; 94US-0293520.
 XX 02-SEP-1994; 94US-0300000.
 XX 08-SEP-1994; 94US-0303039.
 XX 23-SEP-1994; 94US-0311486.
 XX 28-SEP-1994; 94US-0314397.
 XX 03-OCT-1994; 94US-0316771.
 XX 07-OCT-1994; 94US-0319492.
 XX 11-OCT-1994; 94US-0321993.
 XX 04-NOV-1994; 94US-0334847.
 XX 10-NOV-1994; 94US-0337608.
 XX 28-NOV-1994; 94US-0345516.
 XX 16-DEC-1994; 94US-0357577.
 XX 23-DEC-1994; 94US-0363233.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 XX Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 XX Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozymes having modified bases and methods for producing them -
 XX for use in inhibiting disease related genes
 XX Claim 2; Page 243; 407pp; English.

```

XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
XX
XX Query Match 1.1%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 26.7%; Pred. No. 2.9e+02;
XX Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1041 TTATTATTATGTAT 1055
DB 1 UUAUUUUUUUUUU 15

RESULT 242
AAT55817
ID AAT55817 standard; RNA; 15 BP.
XX
XX AAT55817;
XX
XX 25-MAR-2003 (updated)
XX 25-MAR-1997 (first entry)
XX
XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1273).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome;
XX AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB00156.
XX
XX 30-JAN-1995; 95US-0380734.
XX 23-FEB-1994; 94US-0201109.
XX 29-MAR-1994; 94US-0218934.
XX 04-APR-1994; 94US-0222795.
XX 07-APR-1994; 94US-0224483.
XX 15-APR-1994; 94US-0227958.
XX 18-APR-1994; 94US-0228041.
XX 18-MAY-1994; 94US-0245736.
XX 06-JUL-1994; 94US-0271280.
XX 15-AUG-1994; 94US-0291932.
XX 16-AUG-1994; 94US-0291433.
XX 17-AUG-1994; 94US-0292620.
XX 19-AUG-1994; 94US-0293520.
XX 02-SEP-1994; 94US-0300060.
XX 08-SEP-1994; 94US-0303039.

23-SEP-1994; 94US-0311486.
23-SEP-1994; 94US-0311749.
28-SEP-1994; 94US-0314397.
03-OCT-1994; 94US-0316771.
07-OCT-1994; 94US-0319492.
11-OCT-1994; 94US-0321993.
04-NOV-1994; 94US-0334847.
10-NOV-1994; 94US-0337608.
28-NOV-1994; 94US-0345516.
16-DEC-1994; 94US-0357577.
23-DEC-1994; 94US-0363233.
(RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpelesky A, Klsich K, Matulic-adamic J, McSwiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
XX Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them -
XX for use in inhibiting disease related genes
XX
XX Claim 2; Page 243; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
XX mRNA at the nucleotide base position indicated in the DE line.
XX Regions of the mRNA that do not form secondary folding
XX structures and that contain potential hammerhead and hairpin
XX ribozyme cleavage sites were identified by computer analysis.
XX Ribozymes directed against these mRNA sequences were designed and
XX synthesised with modifications that improve their nuclease
XX resistance. The ribozymes are designed to cleave the target
XX sequences and thereby inhibit TNF-alpha expression, making them
XX potentially useful for treating rheumatoid arthritis, septic shock
XX and other inflammatory disorders including psoriasis, as well as
XX for treatment of AIDS.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
XX
XX Query Match 1.1%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 26.7%; Pred. No. 2.9e+02;
XX Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1042 TATTATTATGTAT 1056
DB 1 UUAUUUUUUUUUU 15

RESULT 243
AAT55819
ID AAT55819 standard; RNA; 15 BP.
XX
XX AAT55819;
XX
XX 25-MAR-2003 (updated)
XX 25-MAR-1997 (first entry)
XX
XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1274).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome;
XX AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB00156.
XX
XX 30-JAN-1995; 95US-0380734.
XX 23-FEB-1994; 94US-0201109.
XX 29-MAR-1994; 94US-0218934.
XX 04-APR-1994; 94US-0222795.
XX 07-APR-1994; 94US-0224483.
XX 15-APR-1994; 94US-0227958.
XX 18-APR-1994; 94US-0228041.
XX 18-MAY-1994; 94US-0245736.
XX 06-JUL-1994; 94US-0271280.
XX 15-AUG-1994; 94US-0291932.
XX 16-AUG-1994; 94US-0291433.
XX 17-AUG-1994; 94US-0292620.
XX 19-AUG-1994; 94US-0293520.
XX 02-SEP-1994; 94US-0300060.
XX 08-SEP-1994; 94US-0303039.

```


KW AIDS; ss.
 OS Homo sapiens.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowhira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-351090/45.
 XX
 PT Ribozymes having modified bases and methods for producing them -
 for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 243; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNP-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNP-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
 XX
 Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 26.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 Qy 1043 ATTATTATGATTT 1057

Db
 RESULT 244
 AAT55797
 ID AAT55797 standard; RNA; 15 BP.
 XX
 AC AAT55797;
 XX
 XX
 DT 25-MAR-2003 (updated)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human TNP-alpha hammerhead ribozyme target sequence (nt position 1259).
 XX

KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNP-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX

OS Homo sapiens.
 XX

PN WO9523225-A2.
 XX

PD 31-AUG-1995.
 XX

PF 23-FEB-1995; 95WO-IB00156.
 XX

PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 18-APR-1994; 94US-0228041.
 PR 06-JUL-1994; 94US-0245736.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX

PA (RIBO-) RIBOZYME PHARM INC.
 XX

PI Stinchcomb DT, Chowhira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-351090/45.
 XX

PT Ribozymes having modified bases and methods for producing them -
 for use in inhibiting disease related genes

XX PS Claim 2; Page 243; 407pp; English.

XX CC The present sequence represents a preferred target sequence for an

XX CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha

XX CC mRNA at the nucleotide base position indicated in the DE line.

XX CC Regions of the mRNA that do not form secondary folding

XX CC structures and that contain potential hammerhead and hairpin

XX CC ribozyme cleavage sites were identified by computer analysis.

XX CC Ribozymes directed against these mRNA sequences were designed and

XX CC synthesised with modifications that improve their nuclease

XX CC resistance. The ribozymes are designed to cleave the target

XX CC sequences and thereby inhibit TNF-alpha expression, making them

XX CC potentially useful for treating rheumatoid arthritis, septic shock

XX CC and other inflammatory disorders including psoriasis, as well as

XX CC for treatment of AIDS.

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 Other;

Query Match 1.1%; Score 13.4; DB 1; Length 15;

Best Local Similarity 26.7%; Pred. No. 2.9e+02;

Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1039 ATTATTATTATGT 1053

DB 1 AUUAUUUUUUUU 15

RESULT 245

AAT55799

ID AAT55799 standard; RNA; 15 BP.

AC AAT55799;

XX 25-MAR-2003 (updated)

DT 25-MAR-1997 (first entry)

XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1261).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

XX intercellular adhesion molecule; rel A; tumour necrosis factor;

XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

XX Philadelphia chromosome; inflammation; autoimmune disease;

XX atherosclerosis; myocardial infarction; stroke; restenosis;

XX transplant rejection; rheumatoid arthritis; psoriasis;

XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;

XX human immunodeficiency virus; acquired immune deficiency syndrome;

XX AIDS; ss.

XX Homo sapiens.

OS

XX W09523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 29-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

XX 15-APR-1994; 94US-0228041.

XX 18-MAY-1994; 94US-0245736.

XX 06-JUL-1994; 94US-0271280.

XX 15-AUG-1994; 94US-0291932.

XX 16-AUG-1994; 94US-0291433.

XX 17-AUG-1994; 94US-0252620.

XX 19-AUG-1994; 94US-0293520.

PR 02-SEP-1994; 94US-0300000.

PR 08-SEP-1994; 94US-0303039.

PR 23-SEP-1994; 94US-0311486.

PR 28-SEP-1994; 94US-0311749.

PR 28-SEP-1994; 94US-0314397.

PR 03-OCT-1994; 94US-0316771.

PR 07-OCT-1994; 94US-0319492.

PR 11-OCT-1994; 94US-0321993.

PR 04-NOV-1994; 94US-0334847.

PR 10-NOV-1994; 94US-0337608.

PR 28-NOV-1994; 94US-0345516.

PR 16-DEC-1994; 94US-0357577.

PR 23-DEC-1994; 94US-0363233.

XX (RIBO-) RIBOZYME PHARM INC.

XX PA

XX PI Stinchcomb DT, Chowkira B, Dorenzo A, Draper KG, Dudycz LW;

XX PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;

XX PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;

XX PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;

XX WPI; 1995-351090/45.

XX Ribozyms having modified bases and methods for producing them -

PT for use in inhibiting disease related genes

XX Claim 2; Page 243; 407pp; English.

XX The present sequence represents a preferred target sequence for an

XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha

XX mRNA at the nucleotide base position indicated in the DE line.

XX Regions of the mRNA that do not form secondary folding

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XX potentially useful for treating rheumatoid arthritis, septic shock

XX and other inflammatory disorders including psoriasis, as well as

XX for treatment of AIDS.

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 Other;

Query Match 1.1%; Score 13.4; DB 1; Length 15;

Best Local Similarity 26.7%; Pred. No. 2.9e+02;

Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1041 TTATTATTATGTAT 1055

DB 1 UUAUUUUUUUUUU 15

RESULT 246

AAT55801

ID AAT55801 standard; RNA; 15 BP.

XX AAT55801;

XX 25-MAR-2003 (updated)

DT 25-MAR-1997 (first entry)

XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1262).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

XX intercellular adhesion molecule; rel A; tumour necrosis factor;

XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

XX Philadelphia chromosome; inflammation; autoimmune disease;

XX atherosclerosis; myocardial infarction; stroke; restenosis;

XX transplant rejection; rheumatoid arthritis; psoriasis;

KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

XX Homo sapiens.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-TB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 29-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

XX 15-APR-1994; 94US-0228041.

XX 06-JUL-1994; 94US-0245736.

XX 15-AUG-1994; 94US-0291932.

XX 17-AUG-1994; 94US-0291433.

XX 17-AUG-1994; 94US-0292620.

XX 19-AUG-1994; 94US-0293520.

XX 02-SEP-1994; 94US-0300000.

XX 08-SEP-1994; 94US-0303039.

XX 23-SEP-1994; 94US-0311486.

XX 28-SEP-1994; 94US-0311749.

XX 03-OCT-1994; 94US-0314397.

XX 07-OCT-1994; 94US-0316771.

XX 11-OCT-1994; 94US-0319492.

XX 04-NOV-1994; 94US-0321993.

XX 10-NOV-1994; 94US-0334847.

XX 16-NOV-1994; 94US-0337608.

XX 16-DEC-1994; 94US-0345516.

XX 23-DEC-1994; 94US-0357577.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowhira B, Direnzo A, Draper KG, Dudycz LW;

PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;

PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;

PI Thompson JB, Tracz D, Usman N, Wincott PE, Woolf T;

XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them -

PT for use in inhibiting disease related genes

XX Claim 2; Page 243; 407pp; English.

XX The present sequence represents a preferred target sequence for an

CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha

CC mRNA at the nucleotide base position indicated in the DE line.

CC Regions of the mRNA that do not form secondary folding

CC structures and that contain potential hammerhead and hairpin

CC ribozyme cleavage sites were identified by computer analysis.

CC Ribozymes directed against these mRNA sequences were designed and

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CC resistance. The ribozymes are designed to cleave the target

CC sequences and thereby inhibit TNF-alpha expression, making them

CC potentially useful for treating rheumatoid arthritis, septic shock

CC and other inflammatory disorders including psoriasis, as well as

CC for treatment of AIDS.

CC (Updated on 25-MAR-2003 to correct PI field.)

XX Query Match 1.1%; Score 13.4; DB 1; Length 15;

XX Best Local Similarity 26.7%; Pred. No. 2.9e+02;

XX Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1042 TATTATTATGTAATT 1056
 DB 1 TACCAUUUUUUUUUU 15

RESULT 247

AAT40324

ID AAT40324 standard; DNA; 15 BP.

XX AAT40324;

XX 05-DEC-1996 (first entry)

XX Primer 1a used to optimise DNA cleavage of a ribozyme.

XX Wild type; self-splicing group I intron; large ribosomal RNA precursor;

XX Tetrahymena thermophila; catalysis; enzymatic RNA; food product;

XX anti-viral agent; mutation; personal care product; cleaning agent; ss.

XX Synthetic.

XX WO9531551-A1.

XX 23-NOV-1995.

XX 26-APR-1995; 95WO-US05141.

XX 01-JUL-1994; 94US-0270180.

XX 13-MAY-1994; 94US-0242402.

XX (SCRI) SCRIPPS RES INST.

XX Joyce GF;

XX WPI; 1996-010936/01.

XX Enzymatic RNA molecules having one or more point mutation(s) -

PT improve the enzymatic performance of the molecules.

XX Example 1; Page 96; 209pp; English.

XX The sequences given in AAT40324-26 represent primer sequences that

CC were used to optimise DNA cleavage activity of the enzymatic RNA

CC molecule of the invention. Primer 1a hybridises to the 3' portion

CC of the substrate that becomes attached to the 3' end of the ribozyme.

CC Primer 1b hybridises to the 3' portion of the ribozyme when no substrate

CC or product remains attached. Primer 2 hybridises to the 3' end of the

CC resulting cDNA and introduces the T7 promoter sequence. The self-

CC splicing group I intron of the invention is based on the large ribosomal

CC RNA precursor from Tetrahymena thermophila. The biological function of

CC this molecule is to catalyse its own excision from precursor RNA to

CC produce mature RNA. The Tetrahymena wild type sequence was used in

CC the design of the enzymatic RNA molecules of the invention. A number

CC of mutations are listed in the specification which improve the enzymatic

CC properties of this molecule, e.g. G444A, G191U, U190A and A314G. The

CC modified enzymatic molecules may be used as medical or pharmaceutical

CC agents for use in anti-viral agents, food products, personal care

CC products or cleaning agents.

XX Query Match 1.1%; Score 13.4; DB 1; Length 15;

XX Best Local Similarity 93.3%; Pred. No. 2.9e+02;

XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTATTT 1061

DB 1 TTTATTTATTTATTT 15

RESULT 248

AAT40327/c

ID AAT40327 standard; DNA; 15 BP.
 XX
 AC AAT40327;
 XX
 DT 05-DEC-1996 (first entry)
 XX
 DE Group I intron substrate 3' portion.
 XX
 KW Wild type; self-splicing group I intron; large ribosomal RNA precursor;
 KW Tetrahymena thermophila; catalysis; enzymatic RNA; food product;
 KW anti-viral agent; mutation; personal care product; cleaning agent; ss.
 XX
 OS Synthetic.
 XX
 PN WO9531551-A1.
 XX
 PD 23-NOV-1995.
 XX
 PF 26-APR-1995; 95WO-US05141.
 XX
 PR 01-JUL-1994; 94US-0270180.
 PR 13-MAY-1994; 94US-0242402.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Joyce GF;
 XX
 DR WPI; 1996-010936/01.
 XX
 PT Enzymatic RNA molecules having one or more point mutation(s) -
 PT improve the enzymatic performance of the molecules.
 XX
 PS Example 1; Page 97; 209pp; English.
 XX
 CC The sequences given in AAT40327-30 represent sequences that were used to
 CC optimise DNA cleavage activity of the enzymatic RNA molecule of the
 CC invention. The 3' portion of the substrate was transferred to the 3'
 CC terminal G of the ribozyme and amplification was performed. The product
 CC of the reaction was a molecule which contained the 3' portion of the
 CC substrate attached to the 3' end of the ribozyme. Selection occurred
 CC when a primer was hybridised across the ligation junction and used to
 CC initiate cDNA synthesis. The primer does not bind to unreacted starting
 CC materials and thus led to selective amplification of the catalytically
 CC active RNA's. The self-splicing group I intron of the invention is
 CC based on the large ribosomal RNA precursor from Tetrahymena thermophila.
 CC The biological function of this molecule is to catalyse its own excision
 CC from precursor RNA to produce mature rRNA. The Tetrahymena wild type
 CC sequence was used in the design of the enzymatic RNA molecules of the
 CC invention. A number of mutations are listed in the specification which
 CC improve the enzymatic properties of this molecule, e.g. G444A, G191U,
 CC U190A and A314G. The modified enzymatic molecules may be used as
 CC medical or pharmaceutical agents for use in anti-viral agents, food
 CC products, personal care products or cleaning agents.
 XX
 SQ Sequence 15 BP; 12 A; 0 C; 0 G; 3 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1047 TTTATGATTTATTT 1061
 DB 15 TTTATTTATTTATTT 1
 RESULT 249
 AAT16099/c
 ID AAT16099 standard; DNA; 15 BP.
 XX
 AC AAT16099;
 XX
 DT 15-MAY-1996 (first entry)
 XX

DE Probe ATT-3.
 XX
 KW KM31-7; glutathione reducing protein; nuclear inclusion a;
 KW protease; autolysis; protein fusion; cleavage; chloroindophenol;
 KW oxidative stress; activated oxygen; therapy; probe; ss.
 XX
 OS Synthetic.
 XX
 PN AU9524970-A.
 XX
 PD 25-JAN-1996.
 XX
 PF 13-JUL-1995; 95AU-0024970.
 XX
 PR 07-DEC-1994; 94JP-0303809.
 PR 13-JUL-1994; 94JP-0161053.
 PR 13-SEP-1994; 94JP-0218392.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Kawashima I, Koishi R, Serizawa N, Takahashi T;
 XX
 DR WPI; 1996-117338/13.
 XX
 PT Clover yellow vein virus nuclear inclusion and dichloroindophenol
 PT or oxidised glutathione reducing protein - useful in autolysing
 PT fusion protein expression systems and for treating diseases related
 PT to oxidative stress, or caused by activated oxygen, respectively.
 XX
 PS Example 3; Page 87; 168pp; English.
 XX
 CC DNA probe ATT-3 (AAT16099) is complementary to the AUUUA motif common
 CC to the 3' non-translated region of cytokine mRNAs. It was used to
 CC screen a cDNA library prep'd from human bone marrow stromal
 CC KM-102 cells. A cDNA sequence (AAT16092) coding for a novel
 CC dichloroindophenol- and glutathione-reducing protein, KM31-7
 CC (AA892050), was obt'd. This can be used to treat diseases related to
 CC oxidative stress or caused by activated oxygen.
 XX
 SQ Sequence 15 BP; 11 A; 0 C; 0 G; 4 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1044 TTATTATGATTTATTTA 1058
 DB 15 TTATTATTTATTTA 1
 RESULT 250
 AAV09042
 ID AAV09042 standard; DNA; 15 BP.
 XX
 AC AAV09042;
 XX
 DT 25-JUN-1998 (first entry)
 XX
 DE Primer la for tetrahymena ribozyme L-21.
 XX
 KW Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase;
 KW protease; antiviral agent; gene regulator; immunogenic virus; vaccine;
 KW mutation detection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Tetrahymena sp.
 XX
 PN WO9802583-A1.
 XX
 PD 22-JAN-1998.
 XX
 PF 16-JUL-1997; 97WO-US12394.
 XX

PR 17-JUL-1996; 96US-0682423.

XX (SCRI) SCRIPPS RES INST.

XX Joyce GF;

XX WPI; 1998-110627/10.

XX Catalytic RNA for site-specific cleavage of nucleic acid or
PT hydrolysis of amide bonds - and ribozyme amidase intermediates,
PT useful e.g. as peptidase(s), antiviral agents and gene regulators
XX Example 1; Page 90; 215pp; English.

XX This sequence is a primer for a wild type tetrahymena ribozyme L-21 form.
CC The amplified sequence is an example of a catalytic RNA (I) of the
CC invention, which catalyses site-specific cleavage of nucleic acid under
CC physiological conditions includes a sequence derived from a group I
CC intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide
CC ends are useful as peptidases and proteases, e.g. in wound debridement,
CC clot dissolution, in detergents or as a meat tenderiser. (I) cleave
CC single- and (partly) double-stranded nucleic acids in vitro or in vivo,
CC and are potentially useful as antiviral agents and gene regulators; also
CC to generate defective but still immunogenic viruses (for vaccines);
CC diagnostically to detect mutations in nucleic acid or to identify nucleic
CC acid binding agents; to modulate/terminate reactions initiated by DNA
CC primers; to generate truncated transcripts from DNA; to modulate
CC therapeutic/diagnostic processes using antisense sequences; in DNA
CC fingerprinting and for vector construction. (I) and (II) are produced by
CC in vitro evolution processes that provide better catalytic performance;
CC broader active temperature and pH ranges; new enzymatic activities or
CC specificities; altered recognition sites or co-factor requirement.

XX Sequence 15 BP; 3 A; 0 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTATTT 1061
DB 1 TTTATTTATTTATTT 15

RESULT 251

ID AAH26597 standard; mRNA; 15 BP.

XX AAH26597;

XX 12-NOV-2001 (first entry)

XX Human interferon-alpha gene 3' UTR AU-rich element.

XX Interferon-alpha; human; AU-rich element; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc_feature 2..6 /tag= a

XX /note= "AUUUA motif"

XX misc_feature 6..10 /tag= b

XX /note= "AUUUA motif"

XX misc_feature 10..14 /tag= c

XX /note= "AUUUA motif"

XX WO200164921-A1.

XX 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US06782.

XX 29-FEB-2000; 2000US-0515369.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Fisher PB, Madireddi MT;

XX WPI; 2001-565508/63.

XX Melanoma differentiation associated gene-7 promoter capable of
PT treating cancer comprises directing transcription of heterologous
PT coding sequence encoding tumour suppressor polypeptide positioned
PT downstream, useful for treating cancer
XX Disclosure; Fig 2C; 132pp; English.

XX The present sequence is that of an AU-rich sequence in the 3'
CC untranslated region (3'UTR) of human interferon-alpha mRNA. The
CC presence of AU-rich elements (AREs) in eukaryotic mRNAs correlates
CC with rapid mRNA turnover and post-translational control. The ARE
CC consists of multiple AUUUA motifs or sequences resembling it. A
CC similar ARE sequence is found in the 3' UTR of the human melanoma
CC differentiation associated gene-7 (Mda-7) gene (see AAH26596).
CC The invention provides recombinant expression constructs in which
CC the human Mda-7 promoter (see AAH26595) is operably linked to a
CC coding sequence encoding a tumour suppressor protein. A
CC pharmaceutical composition including the recombinant expression
CC construct is used in a claimed method of treating melanoma,
CC neuroblastoma, astrocytoma, glioblastoma multiforme, cervical
CC cancer, breast cancer, colon cancer, prostate cancer, osteosarcoma,
CC chondrosarcoma or a cancer of the central nervous system.

XX Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1049 TATGTATTTATTTAA 1063
DB 1 UAUUUUUUUUUUAA 15

RESULT 252

ID AAF80978 standard; DNA; 15 BP.

XX AAF80978;

XX 02-MAY-2001 (first entry)

XX PTC52 allele specific oligonucleotide primer SEQ ID 84.

XX Human; prostaglandin-endoperoxide synthase 2; PTC52; cyclooxygenase 2;
XX single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
XX inflammation; PCR primer; ss.

XX Homo sapiens.

XX WO200107662-A1.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US20114.

XX 22-JUL-1999; 99US-0145170.

XX (GENA-) GENAISANCE PHARM INC.

XX Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;

XX WPI; 2001-182805/18.

XX

XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
PT for gene therapy of inflammation and for establishing a genotype or
PT haplotype -
XX
XX Disclosure; Page 23; 118pp; English.
XX
XX This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAF72199. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolate and characterize the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents.
XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 T; 0 other;
SQ
Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1045 TATTATGCTATTAT 1059
Db 1 TATTATTTTATTAT 15
RESULT 253
AAF48964
ID AAF48964 standard; DNA; 15 BP.
XX
XX AAF48964;
DT 30-MAR-2001 (first entry)
DE IGFBP3 oligonucleotide #2384.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
PN WO200078341-A1.
PD 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU00693.
XX
XX 21-JUN-1999; 99US-0140345.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX

PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX Example 7; Page 59; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide. (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3) which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-P45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids,
CC keratosis, neoplasia, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other of
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 2 C; 0 G; 10 T; 0 other;
SQ
Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1520 CTTTATTTTAAAC 1534
Db 1 CTTTATTTTAAAC 15
RESULT 254
AAF48965
ID AAF48965 standard; DNA; 15 BP.
XX
XX AAF48965;
DT 30-MAR-2001 (first entry)
DE IGFBP3 oligonucleotide #2385.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
PN WO200078341-A1.
PD 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU00693.
XX
XX 21-JUN-1999; 99US-0140345.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 PS Example 7; Page 59; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-P45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;
 SQ Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1521 TTATATTTTAACT 1535
 Db 1 TTATATTTTAACT 15
 RESULT 255
 AAF48966
 ID AAF48966 standard; DNA; 15 BP.
 XX AAF48966;
 AC AAF48966;
 DT 30-MAR-2001 (first entry)
 DE IGFBP3 oligonucleotide #2386.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 PD 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI
 XX WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 PS Example 7; Page 59; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects

XX Example 7; Page 59; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-P45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;
 SQ Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1522 TTATATTTTAACT 1536
 Db 1 TTATATTTTAACT 15
 RESULT 256
 AAF48967
 ID AAF48967 standard; DNA; 15 BP.
 XX AAF48967;
 AC AAF48967;
 DT 30-MAR-2001 (first entry)
 DE IGFBP3 oligonucleotide #2387.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 PD 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI
 XX WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 PS Example 7; Page 59; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects

CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-P45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruha, pilaris, seborrheoa, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;
SQ

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1523 TATATTTTAACTTT 1537
DB 1 TATTTTAACTTT 15

RESULT 257
AAT40332/C
ID AAT40332 standard; DNA; 16 BP.
XX AAT40332;
XX
XX
XX 06-DEC-1996 (first entry)
XX
XX DNA cleavage substrate #2 for generation of improved ribozymes.
XX Wild type; self-splicing group I intron; large ribosomal RNA precursor;
XX Tetrahymena thermophila; catalysis; enzymatic RNA; food product;
XX anti-viral agent; mutation; personal care product; cleaning agent; ss.
XX Synthetic.
XX WO9531551-A1.
XX
XX 23-NOV-1995.
XX
XX 26-APR-1995; 95WO-US05141.
XX
XX 01-JUL-1994; 94US-0270180.
XX 13-MAY-1994; 94US-0242402.
XX (SCRI) SCRIPPS RES INST.
XX Joyce GF;
XX WPI; 1996-010936/01.
XX
XX Enzymatic RNA molecules having one or more point mutation(s) -
XX improve the enzymatic performance of the molecules.
XX Example 1; Page 111; 209pp; English.

CC The sequences given in AAT40331-32 represent sequences that were as
CC substrate molecules in experiments for selection of improved catalytic
CC activity of ribozymes. The evolution experiment spanned 10 successive
CC generations and catalytic activity was deduced after each generation.
CC The self-splicing group I intron of the invention is based on the large
CC ribosomal RNA precursor from Tetrahymena thermophila. The biological
CC function of this molecule is to catalyze its own excision from precursor
CC RNA to produce mature rRNA. The Tetrahymena wild type sequence was
CC used in the design of the enzymatic RNA molecules of the invention.
CC A number of mutations are listed in the specification which improve
CC the enzymatic properties of this molecule, e.g. G444A, G191U, U190A and

CC A314G. The modified enzymatic molecules may be used as medical or
CC pharmaceutical agents for use in anti-viral agents, food products,
CC personal care products or cleaning agents.
XX Sequence 16 BP; 13 A; 0 C; 0 G; 3 T; 0 other;
SQ

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTATTT 1061
DB 15 TTTATTTATTTATTT 1

RESULT 258
AAT40329
ID AAT40329 standard; DNA; 16 BP.
XX
XX AAT40329;
XX
XX 05-DEC-1996 (first entry)
XX Improved cleavage group I intron primer 1.
XX Wild type; self-splicing group I intron; large ribosomal RNA precursor;
XX Tetrahymena thermophila; catalysis; enzymatic RNA; food product;
XX anti-viral agent; mutation; personal care product; cleaning agent; ss.
XX Synthetic.
XX WO9531551-A1.
XX
XX 23-NOV-1995.
XX
XX 26-APR-1995; 95WO-US05141.
XX
XX 01-JUL-1994; 94US-0270180.
XX 13-MAY-1994; 94US-0242402.
XX (SCRI) SCRIPPS RES INST.
XX Joyce GF;
XX WPI; 1996-010936/01.
XX
XX Enzymatic RNA molecules having one or more point mutation(s) -
XX improve the enzymatic performance of the molecules.

XX Example 1; Page 98; 209pp; English.
XX The sequences given in AAT40327-30 represent sequences that were used to
XX optimise DNA cleavage activity of the enzymatic RNA molecule of the
XX invention. The 3' portion of the substrate was transferred to the 3'
XX terminal G of the ribozyme and amplification was performed. The product
XX of the reaction was a molecule which contained the 3' portion of the
XX substrate attached to the 3' end of the ribozyme. Selection occurred
XX when a primer was hybridised across the ligation junction and used to
XX initiate cDNA synthesis. The primer does not bind to unreacted starting
XX materials and thus led to selective amplification of the catalytically
XX active RNA's. The self-splicing group I intron of the invention is
XX based on the large ribosomal RNA precursor from Tetrahymena thermophila.
XX The biological function of this molecule is to catalyze its own excision
XX from precursor rRNA to produce mature rRNA. The Tetrahymena wild type
XX sequence was used in the design of the enzymatic RNA molecules of the
XX invention. A number of mutations are listed in the specification which
XX improve the enzymatic properties of this molecule, e.g. G444A, G191U,
XX U190A and A314G. The modified enzymatic molecules may be used as
XX medical or pharmaceutical agents for use in anti-viral agents, food
XX products, personal care products or cleaning agents.
XX Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTT 1061
|||||
DB 1 TTTATTTATTTATTT 15

RESULT 259
AAV09052
ID AAV09052 standard; DNA; 16 BP.
XX
AC AAV09052;
XX
XX 25-JUN-1998 (first entry)
DT
XX
DE Primer 1 for tetrahymena ribozyme L-21.
XX
KW Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase;
KW protease; antiviral agent; gene regulator; immunogenic virus; vaccine;
KW mutation detection; PCR primer; ss.
XX
OS Synthetic.
OS Tetrahymena sp.
XX
XX WO9802583-Al.
XX
XX 22-JAN-1998.
PD
XX
XX 16-JUL-1997; 97WO-US12394.
PF
XX
XX 17-JUL-1996; 96US-0682423.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Joyce GF;
PI
XX
XX WPI; 1998-110627/10.
DR
XX
XX Catalytic RNA for site-specific cleavage of nucleic acid or
PT hydrolysis of amide bonds - and ribozyme amidase intermediates,
PT useful e.g. as peptidase(s), antiviral agents and gene regulators
XX
XX Example 1; Page 92; 215pp; English.
PS
XX
XX This sequence is a primer for a wild type tetrahymena ribozyme L-21 form.
CC The amplified sequence is an example of a catalytic RNA (I) of the
CC invention, which catalyses site-specific cleavage of nucleic acid under
CC physiological conditions includes a sequence derived from a group I
CC intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide
CC ends are useful as peptidases and proteases, e.g. in wound debridement,
CC clot dissolution, in detergents or as a meat tenderiser. (I) cleave
CC single- and (partly) double-stranded nucleic acids in vitro or in vivo,
CC and are potentially useful as antiviral agents and gene regulators; also
CC to generate defective but still immunogenic viruses (for vaccines);
CC diagnostically to detect mutations in nucleic acid or to identify nucleic
CC acid binding agents; to modulate/terminate reactions initiated by DNA
CC primers; to generate truncated transcripts from DNA; to modulate
CC therapeutic/diagnostic processes using antisense sequences; in DNA
CC fingerprinting and for vector construction. (I) and (II) are produced by
CC in vitro evolution processes that provide better catalytic performance;
CC broader active temperature and pH ranges; new enzymatic activities or
CC specificities; altered recognition sites or co-factor requirement.
XX
XX Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTT 1061
|||||
DB 1 TTTATTTATTTATTT 15

Db 1 TTTATTTATTTATTT 15

RESULT 260
AAC65598/c
ID AAC65598 standard; DNA; 16 BP.
XX
XX AAC65598;
AC
XX
XX 14-FEB-2001 (first entry)
DT
XX
XX Human uteroglobin SNP PCR primer HUG-3100AP.
DE
XX
XX Mouse; uteroglobin; immunoglobulin A mediated disease; IGA nephropathy;
KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosis;
KW Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200062795-A2.
FN
XX
XX 26-OCT-2000.
PD
XX
XX 13-APR-2000; 2000WO-US09979.
PF
XX
XX 21-APR-1999; 99US-0130434.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
FA
XX
XX Mukherjee AB, Zheng P, Zhang Z;
PI
XX
XX WPI; 2000-687100/67.
DR
XX
XX Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
PT pulmonary inflammation -
XX
XX Example 12; Page 43; 60pp; English.
PS
XX
XX The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IGA mediated diseases, such as IGA nephropathy,
CC Wegener's granulomatosis, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IGA and the deposition of
CC immune complexes in the kidney.
XX
XX Sequence 16 BP; 1 A; 0 C; 3 G; 12 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1204 ATTATACAAACAAAC 1218
|||||
DB 15 ATTATACAAACAAAC 1

RESULT 261
AAQ78891/c
ID AAQ78891 standard; DNA; 17 BP.
XX
XX AAQ78891;
AC
XX
XX 25-MAR-2003 (updated)
DT
XX
XX 18-DEC-1995 (first entry)
DT
XX
XX Humicola grisea glucoamylase hybridization probe.
DE
XX
XX Glucoamylase; DNA probe; gene cloning; protein secretion; ss.
KW
XX
XX Synthetic.
OS
XX

PN BP625577-A1.
XX 23-NOV-1994.
XX 27-AUG-1986; 94EP-0201751.
XX 29-AUG-1985; 85US-0771374.
PR 07-JUL-1986; 86US-0882224.
PR 27-AUG-1986; 86EP-0306624.
XX (GENEV) GENENCOR INT INC.
PA Berka RM, Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
PI WPI; 1994-359750/45.
XX Vectors and DNA for expressing polypeptide(s) in filamentous fungi
PT - include secretory signal sequences that are native or foreign to
PT heterologous polypeptide(s), such as chymosin or glucosylase.
XX Example 9A3; Page 22; 50pp; English.
XX The DNA probe and corresponding probes covering the degenerate
CC sites (AAQ7885-Q7880) correspond to amino acids 17-22 of the
CC H. grisea glucosylase peptide GRI (AA62933), and are used as
CC hybridization probes to detect and isolate H. grisea glucosylase
CC DNA in a Southern blot. Resulting genomic DNA fragments are
CC excised and cloned in plasmid pKSH1. This illustrates the main
CC claims of the patent, i.e. a vector containing (i) DNA encoding
CC a heterologous polypeptide (chymosin, prochymosin, preprochymosin,
CC Aspergillus niger glucosylase, H. grisea glucosylase, or Mucor
CC miehei carboxyl protease), and (ii) a secretory signal peptide,
CC and a filamentous fungus (Aspergillus, Trichoderma, Neurospora,
CC Podospora, Endothia, Mucor, Cochliobolus or Pyricularia, especially
CC A. nidulans, A. awamori or T. reesei) transformed with the vector
CC for recombinant protein (enzyme) production.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 17 BP; 11 A; 2 C; 0 G; 3 T; 1 other;
SQ Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1047 TTTATGTAATTTATTT 1061
DB 17 TTTATGTAATTTATTT 3
RESULT 262
AAQ92084
ID AAQ92084 standard; cDNA; 17 BP.
XX AC AAQ92084;
XX 25-MAR-2003 (updated)
DT 07-JAN-1996 (first entry)
XX Renilla reniformis luciferase DNA probe-1.
XX Luciferase; enzyme; bioluminescence; luminescence; label; DNA probe;
XX antibody; oligonucleotide; ss.
XX Synthetic.
XX US5418155-A.
XX 23-MAY-1995.
XX 14-DEC-1993; 93US-0167650.
XX 29-DEC-1989; 89US-0458952.
PR

PR 20-AUG-1992; 92US-0933017.
PR 17-JUN-1993; 93US-0079700.
PR 14-DEC-1993; 93US-0167650.
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX Cormier MJ, Lorenz WW;
XX WPI; 1995-199741/26.
XX New recombinant Renilla luciferase polypeptide - used as a
PT luminescent tag, partic in bio-luminescence assays and for the prodn
PT of antibodies
XX Disclosure; Fig. 4; 18pp; English.
XX This 17-mer oligonucleotide DNA probe, along with Probe-2 (AAQ92085)
CC are used to screen an R. reniformis cDNA library to isolate cDNA
CC encoding Renilla luciferase. The luciferase was then expressed
CC using E. coli.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct DR field.)
XX Sequence 17 BP; 6 A; 0 C; 2 G; 9 T; 0 other;
SQ Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1259 AAATAATTTTATTTAGT 1273
DB 3 AAATAATTTTATTTGT 17
RESULT 263
AAAT81505/c
ID AAAT81505 standard; RNA; 17 BP.
XX AC AAAT81505;
XX 14-DEC-1997 (first entry)
DT Human c-myb hammerhead ribozyme target sequence (nt. position 2712).
XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
XX smooth muscle cell; hyperproliferation; restenosis; cancer;
XX c-myb; coronary angioplasty; ss.
XX Homo sapiens.
XX WO9531541-A2.
XX 23-NOV-1995.
XX 18-MAY-1995; 95WO-US06368.
XX 13-JAN-1995; 95US-0373124.
PR 18-MAY-1994; 94US-0245466.
XX (RIBO-) RIBOZYME PHARM INC.
XX Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
XX WPI; 1996-010927/01.
XX New enzymatic nucleic acid molecules - which cleave RNA produced by
XX e.g. c-myb, for treating restenosis or cancer
XX Claim 1; Page 77; 128pp; English.
XX The present sequence represents the preferred target sequence for an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the human c-myb sequence at the base position indicated in the

CC descriptor line. The c-myb sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm, and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised and
 CC their activities optimised by either varying the length of the binding
 CC arms or by modification to prevent degradation by nucleases.
 CC The ribozymes cleave the c-myb sequence and can be used to prevent
 CC smooth muscle cell hyperproliferation in restenosis, especially after
 CC coronary angioplasty, and in cancers.

XX SQ Sequence 17 BP; 8 A; 0 C; 0 G; 9 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. NO. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1617 AAAATATAAATTGTT 1631
 Db |||||
 16 AAAATATAAATTGTT 2

RESULT 264

AAAX75068/C
 ID AAX75068 standard; RNA; 17 BP.

XX AC AAX75068;

XX DT 28-JUL-1999 (first entry)

XX DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #596.

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;

XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

XX KW foetal liver kinase 1; ss.

XX OS Mus sp.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US17480.

XX PF 11-JAN-1996; 96US-0584040.

XX PR 26-OCT-1995; 95US-0005974.

XX PS (CHIR) CHIRON CORP.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX DR WPI; 1997-259017/23.

XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or

XX PT mRNA stability - useful for treating e.g. tumour angiogenesis,

XX PT psoriasis, rheumatoid arthritis, etc., in a human patient

XX PS Claim 4; Page 173; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.

XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. NO. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 ACACAAACACACAA 630
 Db |||||
 15 ACACAAACACACAA 1

RESULT 265

AAAX70035
 ID AAX70035 standard; RNA; 17 BP.

XX AC AAX70035;

XX DT 28-JUL-1999 (first entry)

XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1330.

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;

XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

XX KW foetal liver kinase 1; ss.

XX OS Homo sapiens.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US17480.

XX PF 11-JAN-1996; 96US-0584040.

XX PR 26-OCT-1995; 95US-0005974.

XX PS (CHIR) CHIRON CORP.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX DR WPI; 1997-259017/23.

XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 XX PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 XX PT psoriasis, rheumatoid arthritis, etc., in a human patient

XX PS Claim 4; Page 86; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.

XX SQ Sequence 17 BP; 9 A; 2 C; 0 G; 6 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. NO. 3.3e+02;
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 803 ATAAAGTCAAAATTA 817
 Db |||||
 2 AUAACUCAAAUUA 16

RESULT 266

AAK69549/C
ID AAK69549 standard; RNA; 17 BP.
AC
XX
AC AAK69549;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #844.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
XX (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 72; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK67275 to AAK75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 7 A; 3 C; 2 G; 5 U; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 749 TAGAATGATATTT 763
DB 17 TAGAATGATATTT 3
RESULT 267
AAK60263/c
ID AAK60263 standard; DNA; 17 BP.
XX
AC AAK60263;
XX
XX 19-OCT-1997 (first entry)
DT
XX ASO 2184dAN wild-type sequence of cystic fibrosis mutation.
DE
XX Multiplex allele-specific diagnostic assay; MASDA;
KW allele-specific oligonucleotide; ASO; polymorphism;
KW

genetic disease; diagnosis; cystic fibrosis; ss.
XX
OS Synthetic.
XX
PN WO9710366-A2.
XX
PD 20-MAR-1997.
XX
PF 13-SEP-1996; 96WO-US14842.
XX
PR 13-SEP-1996; 96WO-US14842.
XX
PA (GENZ) GENZYME CORP.
XX Shuber AP;
PI
XX WPI; 1997-202258/18.
XX
PT Identifying genetic alterations or target sequences in nucleic acid
PT samples - useful for detecting genetic alterations associated with a
PT disease, e.g. cystic fibrosis and sickle cell anaemia
XX
PS Example 2; Page 42; 85pp; English.
XX
CC Allele-specific oligonucleotides (ASOs) (AAT60210-41) representing
CC known cystic fibrosis mutations, and corresponding ASOs (AAT60242-70)
CC representing wild-type sequences, are examples of ASOs that can be
CC used in a multiplex allele-specific diagnostic assay (MASDA) that
CC has the capacity to analyse over 500 samples of a large number of
CC mutations (over 100) in a single assay. Target DNA is immobilised
CC to a solid support and interrogated in combinatorial fashion with a
CC mixture of mutation-specific ASOs in solution. The ASO(s)
CC corresponding to the specific mutation(s) present in the sample is
CC hybrid-selected from the pool, and the mutation(s) is identified.
CC MASDA can be used to detect genetic alterations associated with
CC genetic disorders, to identify genetic polymorphisms, to determine
CC the molecular basis of genetic diseases, or for high-resolution
CC identification of disease-causing microorganisms.
XX
SQ Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1207 AACCAACAAACAAT 1221
DB 16 AACCAACAAACAAT 2
RESULT 268
AAK21205
ID AAK21205 standard; RNA; 17 BP.
XX
AC AAK21205;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4431.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.

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XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99WO-US06507.
XX PR 27-MAR-1998; 98US-0079678.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX DR WPI; 1999-591315/50.
XX PT Novel ribozymes for modulating the synthesis, expression and/or
XX PT stability of an mRNA encoding an angiogenic factors
XX PS Claim 55; Page 193; 305pp; English.
XX CC The present invention describes enzymatic cleave RNA molecules with
XX CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX CC the invention are used for modulating the synthesis, expression and/or
XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,
XX CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX CC especially used to treat cancer, diabetic retinopathy, age related
XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as
XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX CC integrin subunit alpha-6, or integrin subunit beta-3.
XX SQ Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 33.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1524 ATATTTTAACTTTA 1538
DB 3 AUAUUUUUACUUUA 17

RESULT 269
AA21206
ID AAA21206 standard; RNA; 17 BP.
XX AC AAA21206;
XX DT 19-JUN-2000 (first entry)
XX DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4432.
XX KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX KW hammerhead ribozyme; angiogenic factor; Cytostatic; antidiabetic;
XX KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX KW age related macular degeneration; inflammation; neovascular glaucoma;
XX KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;

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XX KX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX OS Homo sapiens.
XX PN WO9950403-A2.
XX XX 07-OCT-1999.
XX PF 24-MAR-1999; 99WO-US06507.
XX PR 27-MAR-1998; 98US-0079678.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX DR WPI; 1999-591315/50.
XX PT Novel ribozymes for modulating the synthesis, expression and/or
XX PT stability of an mRNA encoding an angiogenic factors
XX PS Claim 55; Page 193; 305pp; English.
XX CC The present invention describes enzymatic cleave RNA molecules with
XX CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX CC the invention are used for modulating the synthesis, expression and/or
XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,
XX CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX CC especially used to treat cancer, diabetic retinopathy, age related
XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as
XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX CC integrin subunit alpha-6, or integrin subunit beta-3.
XX SQ Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 33.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1524 ATATTTTAACTTTA 1538
DB 2 AUAUUUUUACUUUA 16

RESULT 270
AAA21207
ID AAA21207 standard; RNA; 17 BP.
XX AC AAA21207;
XX DT 19-JUN-2000 (first entry)
XX DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4433.
XX KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX KW hammerhead ribozyme; angiogenic factor; Cytostatic; antidiabetic;

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XX AC AAA22695;
XX ID 19-JUN-2000 (first entry)
XX DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5921.
XX KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX KW age related macular degeneration; inflammation; neovascular glaucoma;
XX KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX OS Homo sapiens.
XX PN WO9950403-A2.
XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99WO-US06507.
XX PR 27-MAR-1998; 98US-0079678.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX PI WPI; 1999-591315/50.
XX DR Novel ribozymes for modulating the synthesis, expression and/or
XX PT stability of an mRNA encoding an angiogenic factors
XX PS Claim 54; Page 236; 305pp; English.
XX CC The present invention describes enzymatic cleavage of nucleic acid molecules with
XX CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX CC hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3
XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX CC corresponding target sequences. AAA17685 to AAA18185 and AAA19087 to
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19085
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA21688 represent their corresponding target sequences;
XX CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX CC the invention are used for modulating the synthesis, expression and/or
XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,
XX CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX CC especially used to treat cancer, diabetic retinopathy, age related
XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as
XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX CC integrin subunit alpha-6, or integrin subunit beta-3.
XX SQ Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;

```

```

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

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Qy 1040 TTTATTATTATGTA 1054
Db 3 UUUUUUUUUUUUUA 17

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RESULT 273
AAF02054/c
ID AAF02054 standard; DNA; 17 BP.
XX AC AAF02054;
XX DE 16-FEB-2001 (first entry)
XX KW Hammerhead ribozyme substrate #349.
XX DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO2000061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX PI WPI; 2000-647423/62.
XX DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 37; Page 63; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TP-1, the GATA
XX CC transcription factor gene, IRP-2 and/or the CAAT Displacement
XX CC Protein (CDP). Inhibition of the repressors removes prevents
XX CC inhibition (and consequently increases expression of) genes involved in
XX CC the production of erythropoietin, granulocyte colony stimulating factor
XX CC protein and interferon alpha.
XX SQ Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1004 AACATTAATTTATTTT 1018
Db 15 AAAATAAATTTATTTT 1
RESULT 274
AAF04949
ID AAF04949 standard; DNA; 17 BP.
XX AC AAF04949;
XX DE 16-FEB-2001 (first entry)
XX KW Hammerhead ribozyme substrate #2465.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO2000061729-A2.

```

XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 4; Page 112; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
XX CC protein (CDP). Inhibition of the repressors removes prevents
XX CC inhibition (and consequently increases expression of) genes involved in
XX CC the production of erythropoietin, granulocyte colony stimulating factor
XX CC protein and interferon alpha.
XX CC Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;
XX CC
XX CC Query Match 1.1%; Score 13.4; DB 1; Length 17;
XX CC Best Local Similarity 93.3%; Pred. No. 3.3e+02;
XX CC Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC 632 AATTTTGAATATA 646
XX CC |||||
XX CC 3 AATTTTGAATATA 17
XX CC
XX CC RESULT 275
XX CC ID AAF05525 standard; DNA; 17 BP.
XX CC AC AAF05525;
XX CC DT 16-FEB-2001 (first entry)
XX CC DE Hammerhead ribozyme substrate #2744.
XX CC KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX CC KW interferon alpha; ss.
XX CC OS Homo sapiens.
XX CC PN W0200061729-A2.
XX CC PD 19-OCT-2000.
XX CC PF 11-APR-2000; 2000WO-US09721.
XX CC PR 12-APR-1999; 99US-0129390.
XX CC PA (RIBO-) RIBOZYME PHARM INC.
XX CC PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX CC DR WPI; 2000-647423/62.
XX CC PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX CC PT useful for producing e.g. granulocyte colony stimulating factor
XX CC PT protein, interferon alpha and erythropoietin -
XX CC PS Claim 18; Page 118; 164pp; English.

XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
XX CC protein (CDP). Inhibition of the repressors removes prevents
XX CC inhibition (and consequently increases expression of) genes involved in
XX CC the production of erythropoietin, granulocyte colony stimulating factor
XX CC protein and interferon alpha.
XX CC Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
XX CC
XX CC Query Match 1.1%; Score 13.4; DB 1; Length 17;
XX CC Best Local Similarity 93.3%; Pred. No. 3.3e+02;
XX CC Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC 626 ACAATTAATTTTGA 640
XX CC |||||
XX CC 3 ACTAATTAATTTTGA 17
XX CC
XX CC RESULT 276
XX CC ID ABV80424 standard; DNA; 17 BP.
XX CC AC ABV80424;
XX CC DT 03-JAN-2003 (first entry)
XX CC DE Human HTPL scanning oligonucleotide SEQ ID 1670.
XX CC KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX CC KW human testis expressed patched like protein; testis; adrenal; liver;
XX CC KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX CC KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX CC OS Homo sapiens.
XX CC PN EP1229046-A2.
XX CC PD 07-AUG-2002.
XX CC PF 28-JAN-2002; 2002EP-0001167.
XX CC PR 30-JAN-2001; 2001WO-US00663.
XX CC PR 30-JAN-2001; 2001WO-US00664.
XX CC PR 30-JAN-2001; 2001WO-US00665.
XX CC PR 30-JAN-2001; 2001WO-US00667.
XX CC PR 30-JAN-2001; 2001WO-US00668.
XX CC PR 30-JAN-2001; 2001WO-US00669.
XX CC PR 23-MAY-2001; 2001US-0864761.
XX CC PR 09-OCT-2001; 2001US-0327898.
XX CC PA (ABOM-) ABOMICA INC.
XX CC PI Zhan J;
XX CC DR WPI; 2002-676582/73.
XX CC PT Novel isolated human testis expressed patched like protein (HTPL),
XX CC PT useful for identifying agonist and antagonist and specific binding
XX CC PT partners, and for treating subjects having defects in HTPL -
XX CC PS Example 2; Page 282; 718pp; English.
XX CC
XX CC The present invention relates to human testis expressed patched like
XX CC protein (HTPL), see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
XX CC has two isoforms, with a few single base pair differences between the
XX CC two. One of the single base pair changes introduces a premature stop
XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX CC shares an overall structure organisation with the patched protein. The
XX CC shared structural features strongly imply that HTPL plays a role similar
XX CC to that of patched, and is a potential tumour suppressor. HTPL is

The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and AB938519 to AB938520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The

Claim 4: Page 63; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates
PS expression of an Ets-related gene (EREG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration.

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with RNA. (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.

SQ Sequence 17 BP; 8 A; 2 C; 1 G; 6 U; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1504 ATTTTAAATACAAG 1518
 |||||
 DB 15 ATTTTAAATACAAG 2

RESULT 279
 ABK17632/c
 ID ABK17632 standard; RNA, 17 BP.
 AC ABK17632;
 XX
 XX 09-APR-2002 (first entry)
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 279.
 DE
 DE Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic degeneration; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNase; inozyme;
 KW ambrzyme.
 OS Homo sapiens.
 XX
 XX WC200188124-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US15866.
 XX
 XX 16-MAY-2000; 2000US-0572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber

PT syndrome
 XX Claim 4; Page 63; 149pp; English.
 PS
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with RNA. (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.

SQ Sequence 17 BP; 7 A; 2 C; 2 G; 6 U; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1504 ATTTTAAATACAAG 1518
 |||||
 DB 15 ATTTTAAATACAAG 1

RESULT 280
 ABA02551/c
 ID ABA02551 standard; DNA, 17 BP.
 AC ABA02551;
 XX
 XX 26-MAR-2002 (first entry)
 DE Human ADAMTS-M PCR primer (reverse).
 DE
 DE Osteoarthritis; rheumatoid arthritis; inflammatory bowel disease;
 KW Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection;
 KW cachexia; allergy; cancer; leukaemia; lymphoma; osteoporosis;
 KW atherosclerosis; congestive heart failure; myocardial infarction; stroke;
 KW neurodegenerative disease; autoimmune disorder; Huntington's;
 KW Parkinson's; migraine; pain; depression; multiple sclerosis; burn;
 KW infertility; diabetic shock; gene therapy; ADAMTS-M; PCR; primer; ss;
 KW A Disintegrin And Metalloprotease; thrombospondin domain.
 XX
 XX Homo sapiens.
 OS
 XX BP1152055-A1.
 XX
 XX 07-NOV-2001.
 XX
 XX 24-APR-2001; 2001EP-0303706.
 XX
 XX 27-APR-2000; 2000US-200040P.
 XX
 XX (PFIZ) PFIZER PROD INC.
 XX
 XX Buckbinder L, Mitchell PG, Wachtmann TS, Walsh RT;

XX WPI; 2002-084275/12.

XX New polynucleotide, useful in gene therapy, particularly for treating

PT or preventing e.g. arthritis, Crohn's disease, Alzheimer's disease and

PT organ transplant toxicity and rejection, comprises ADAMTS

PT polynucleotide and encoded polypeptide.

XX Example; Page 13; 31pp; English.

XX The present sequence represents a PCR primer used to screen a panel of

CC CDNA libraries to determine a source for further cloning of novel

CC ADAMTS genes. A PCR product that was obtained (given in ABA02549) that

CC encodes the ADAMTS-M protein (AB04153) that exhibits the characteristics

CC of the ADAM (A Disintegrin And Metalloprotease) family of

CC metalloproteases, and contains a thrombospondin domain (TS). The

CC specification describes a newly isolated polynucleotide, comprising a

CC nucleotide sequence encoding an ADAMTS-M polypeptide as given in the

CC specification, or a metalloproteinase, disintegrin domain, prodomain or

CC its thrombospondin submotif. The polynucleotide, polypeptide and agent

CC are useful for manufacturing a medicament for treating a subject in need

CC of altering activity or expression of ADAMTS-M. The polynucleotide,

CC ADAMTS-M polypeptide and agent are useful for manufacturing a medicament

CC for treating arthritis (osteoarthritis and rheumatoid arthritis), disease,

CC inflammatory bowel disease, Crohn's disease, asthma, Alzheimer's disease,

CC organ transplant toxicity and rejection, cachexia, allergy, cancer (e.g.

CC solid tumour cancer including colon, breast, lung, prostate, brain or

CC haematopoietic malignancies including leukaemia and lymphoma),

CC myocardial infarction, stroke, head trauma, spinal cord injury,

CC neurodegenerative disease, autoimmune disorders, Huntington's disease,

CC Parkinson's disease, migraine, pain, depression, multiple sclerosis,

CC abnormal wound healing, burns, infertility or diabetic shock. The

CC polynucleotide and polypeptide are also useful for diagnosing the

CC diseases above. The polynucleotide is particularly useful in gene therapy

CC for treating the diseases cited above.

XX

SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 3.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 754 TGTGATATTGGAGC 768

DB 15 TGTGATATTGGAGC 1

RESULT 281

ABT34735

ID ABT34735 standard; DNA; 17 BP.

XX

AC ABT34735;

XX

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 372.

DE

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

KW schizophrenia; protein chip; gene therapy; tumour suppression;

KW human fukutin; ds.

XX

OS Homo sapiens.

XX

XX WO2003025175-A2.

XX

XX 27-MAR-2003.

PD

XX 17-SEP-2002; 2002WO-IB04208.

XX

PF 17-SEP-2001; 2001FR-0011978.

XX

PR 17-SEP-2001; 2001FR-0011978.

XX

XX (MOLE-) MOLECULAR ENGINES LAB.

PA (MOLE-) MOLECULAR ENGINES LAB.

XX

PI Telerman A, Amson R, Tuijnder M;

XX

XX WPI; 2003-313353/30.

XX

PT New isolated nucleic acid, useful for treating viral diseases

PT associated with tumors and cell degeneration, also related

PT polypeptides, antibodies and transfected cells

XX

XX Disclosure; Page 77; 720pp; French.

XX

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

CC given in the specification, a sequence containing at least 15

CC consecutive nucleotides from the 17 mer sequence, a sequence with, after

CC optimal alignment, at least 80 % identity to the 17 mer sequence, a

CC sequence that hybridizes to them under highly stringent conditions, or

CC the complement of any of them, or the corresponding RNA. The novel

CC isolated nucleic acids of the invention are useful as probes and primers

CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,

CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,

CC and for production of recombinant polypeptides. Any of the nucleic acids,

CC polypeptides, vectors containing the nucleic acids, cells containing the

CC vector or antibodies directed against the polypeptides are useful for

CC preparation of pharmaceuticals for prevention and/or treatment of viral

CC diseases that are characterised by development of tumours or cell

CC degeneration, specifically cancer but also Alzheimer's disease and

CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and

CC both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene

CC therapy. This polynucleotide sequence represents a tumour suppression

CC related human fukutin oligonucleotide of the invention.

XX

SQ Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 3.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 534 TCAGTAACACATGAA 548

DB 3 TCAGTAACACATGAA 17

RESULT 282

ABT35038/C

ID ABT35038 standard; DNA; 17 BP.

XX

AC ABT35038;

XX

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 675.

DE

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

KW schizophrenia; protein chip; gene therapy; tumour suppression;

KW human fukutin; ds.

XX

OS Homo sapiens.

XX

XX WO2003025175-A2.

XX

XX 27-MAR-2003.

PD

XX 17-SEP-2002; 2002WO-IB04208.

XX

PF 17-SEP-2001; 2001FR-0011978.

XX

PR 17-SEP-2001; 2001FR-0011978.

XX

XX (MOLE-) MOLECULAR ENGINES LAB.

P1 Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 DR
 XX
 PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 PS Disclosure; Page 113; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 9 A; 1 C; 3 G; 4 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1237 ATTTTCATTTTCAGAT 1251
 DB 16 ATTTTTCATTTTCAGAT 2
 RESULT 283
 ABT39610
 ID ABT39610 standard; DNA; 17 BP.
 XX
 AC ABT39610;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 5247.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PP 17-SEP-2002; 2002WO-IB04208.
 XX
 PR 17-SEP-2001; 2001FR-0011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 PS Disclosure; Page 113; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 9 A; 1 C; 3 G; 4 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1237 ATTTTCATTTTCAGAT 1251
 DB 16 ATTTTTCATTTTCAGAT 2
 RESULT 283
 ABT39610
 ID ABT39610 standard; DNA; 17 BP.
 XX
 AC ABT39610;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 5247.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PP 17-SEP-2002; 2002WO-IB04208.
 XX
 PR 17-SEP-2001; 2001FR-0011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 PS Disclosure; Page 647; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 6 A; 1 C; 2 G; 8 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1149 TTATTTTAGATTA 1163
 DB 3 TCATTTTAGATTA 17
 RESULT 284
 ABZ61156
 ID ABZ61156 standard; RNA; 17 BP.
 XX
 AC ABZ61156;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNzyme substrate #1268.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 XX anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PP 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 XX
 PR 06-JUN-2001; 2001US-296249P.
 XX
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.

CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ69889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66924, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.

XX

SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 U; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1332 TCCAGTCTGTGCAT 1346
|||||
Db 15 TCCAGTCTGTGCT 1

RESULT 286
AAA63708
ID AAA63708 standard; DNA; 18 BP.
XX
AC AAA63708;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCR primer used to amplify a fragment of the FRI locus.
XX
KW H51; one locus-FRIGIDA; FRI gene; flowering time; blotting;
XX flower initiation; stem elongation; flower production; PCR primer; ss.
XX
OS Arabidopsis sp.
XX
PN W0200045358-A2.
XX
PD 10-AUG-2000.
XX
PF 25-JAN-2000; 2000WO-GB00197.
XX
PR 05-FEB-1999; 99GB-0002660.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Johanson U, West J, Dean C;
XX WPI; 2000-532899/48.
DR
PT New nucleic acid derived from the FRI locus of a plant, e.g.
PT Arabidopsis, encoding a polypeptide capable of specifically altering
PT the flowering time of a plant -
XX
PS Example 2; Page 43; 73pp; English.
XX

PCR primers AAA63688-A63724 were used to amplify a fragment of the (late
flowering) H51 FRI (one locus-FRIGIDA) locus of Arabidopsis. The
FRI gene encodes a polypeptide capable of specifically altering the
flowering time of a plant. The FRI polynucleotide is used to transform
plants, so that the flowering time of a plant is altered. This is used,
for example, for plants in which the leaves or tubers are a commercial
product, where it is desirable to avoid 'blotting' (initiation of
flowers and stem elongation) at too early a stage. Conversely, it may
be desirable to alter flowering under certain circumstances e.g. to vary
flower production across the seasons.

XX

SQ Sequence 18 BP; 3 A; 4 C; 3 G; 8 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps

OY 1545 TTATTGTCCTCC 1559

```

Db      ||| ||||| ||||| |||
        4 TTTCATGCTCC 18

RESULT 287
AAZ35889
ID     AAZ35889 standard; DNA; 18 BP.
XX
AC     AAZ35889;
XX
DT     03-FEB-2000 (first entry)
XX
DE     Human sentrin phosphorothioate antisense oligonucleotide SEQ ID NO:31.
XX
KW     Human; sentrin; antisense oligonucleotide; phosphorothioate;
KW inhibition; modulation; expression; diagnosis; ss.
XX
OS     Synthetic.
XX
OS     Homo sapiens.
XX
FH     Key                      Location/Qualifiers
FT     modified_base          1...18
FT                                     /*tag= a
FT                                     /note= "phosphorothioate linkages"
XX
PN     US5985664-A.
XX
PD     16-NOV-1999.
XX
XX     17-DEC-1998;    98US-0213768.
XX
PR     17-DEC-1998;    98US-0213768.
XX
PA     (ISIS-) ISIS PHARM INC.
XX
PI     Baker BP,   Cowsert LM;
XX
DR     WPI; 2000-022284/02.
XX
PT     Antisense compound which modulates human sentrin expression, useful for
PT treating diseases associated with sentrin expression -
XX
PS     Example 15; Column 38; 29pp; English.
XX
CC     The present invention describes an antisense compound (I) 8-30
CC nucleotides long targeted to a nucleic acid molecule encoding human
CC sentrin. The antisense compound comprises a phosphorothioate antisense
CC oligonucleotide which inhibits expression of human sentrin. (I) is
CC useful for inhibiting expression of sentrin in human cells or tissues
CC in vitro, for treating humans or other animals suspected of having or
CC being prone to a disease associated with sentrin expression. (I) can
CC also be used for research or diagnostic purposes. The present
CC sequence represents a human sentrin phosphorothioate antisense
CC oligonucleotide from the present invention.
XX
SQ     Sequence 18 BP; 8 A; 4 C; 1 G; 5 T; 0 other;

Query Match           1.1%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1179 GATAAATTCAATCA 1193
         ||||| |||||
Db      1 GATAACTTCAATCA 15

RESULT 288
AAF92967
ID     AAF92967 standard; DNA; 18 BP.
XX
AC     AAF92967;
XX
DT     17-MAY-2001 (first entry)
XX

```

XX 07-MAY-1999; 99US-0306970.
 XX (ICOS-) ICOS CORP.
 XX Dietsch GN, Peterman GM, Yu AS;
 XX WPI; 2002-673986/72.
 XX Preventing diabetes mellitus comprises administering a platelet
 PT activating factor acetylhydrolase product to a subject at risk of
 PT developing the disease -
 XX
 XX Disclosure; Page 14; 22pp; English.
 XX The invention relates to a method for preventing diabetes mellitus
 CC comprising administering a platelet activating factor acetylhydrolase
 CC (PAF-AH) product to a subject at risk of developing diabetes mellitus.
 CC The method is also used to slow the progression of diabetes mellitus in a
 CC patient suffering from the disease. This sequence represents a
 CC Saccharomyces cerevisiae PAF-AH DNA related oligonucleotide.
 XX
 XX Sequence 18 BP; 4 A; 1 C; 4 G; 9 T; 0 other;
 SQ
 Query Match 1.18; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1282 ATTATTGTTATCTG 1296
 |||||
 DB 3 ATTATTGTTATCTG 17
 RESULT 290
 AAT66013/c
 ID AAT66013 standard; DNA; 19 BP.
 XX
 AC AAT66013;
 XX
 DT 25-MAR-2003 (updated)
 DT 18-JUN-1997 (first entry)
 XX
 DE Primer #2 to amplify repeat sequence marker Mfd108.
 XX
 KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.
 XX
 OS Synthetic.
 XX
 PN US582979-A.
 XX
 PD 10-DEC-1996.
 XX
 PF 04-APR-1994; 94US-0222177.
 XX
 PR 05-SEP-1991; 91US-0754351.
 PR 21-APR-1989; 89US-0341562.
 PR 04-APR-1994; 94US-0222177.
 XX
 PA (MARS-) MARSHFIELD CLINIC.
 XX
 PI Weber JL;
 XX
 DR WPI; 1997-042299/04.
 XX
 PT Detection of polymorphic genetic markers of the form
 PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
 XX
 PS Claim 7; Column 13-14; 186pp; English.
 XX
 CC The invention relates to the isolation of polymorphic repeat sequences

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect these
 CC repeats, especially for use in e.g. paternity or maternity testing,
 CC human genetic analysis such as linkage analysis of genetic disease,
 CC commercial animal or plant breeding or pedigree analysis. Clones
 CC containing the repeat sequences were isolated by hybridisation of
 CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
 CC probe. Over 100 repeat blocks were isolated. The primers
 CC AAT65798-T66047 were used to PCR amplify the inserts from the isolated
 CC clones containing the repeat sequences. The primers AAT66012-3 were used
 CC to amplify the repeat sequence marker clone Mfd108 (AAT65779).
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 19 BP; 4 A; 10 C; 1 G; 4 T; 0 other;
 SQ
 Query Match 1.11%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 3.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 957 AGTGATGTTGTCAGG 971
 |||||
 DB 17 AGTGATGTTGTCAGG 3
 RESULT 291
 AAX02160
 ID AAX02160 standard; DNA; 19 BP.
 XX
 AC AAX02160;
 XX
 DT 23-APR-1999 (first entry)
 XX
 DE Human IVS17 3'-acceptor splice site PCR primer #8.
 XX
 KW IVS17 acceptor splice site; PCR primer; detection; base-pair mutation;
 KW heteroduplex; homoduplex; migration; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5874212-A.
 XX
 PD 23-FEB-1999.
 XX
 PF 06-JUN-1995; 95US-0468551.
 XX
 PR 06-JUN-1995; 95US-0468551.
 PR 13-MAY-1993; 93US-0061574.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Garguly A, Prockop DJ, Rock MJ;
 XX
 DR WPI; 1999-179967/15.
 XX
 PT Detection of nucleic acid mutations - by electrophoresis in
 PT polyacrylamide gel that distinguishes heteroduplexes from
 PT homoduplexes
 XX
 PS Disclosure; Column 5; 16pp; English.
 XX
 CC AAX02153-X02161 are primers used in a method for detecting one or more
 CC base-pair mutations in a nucleic acid sequence by differentiating
 CC heteroduplexes from homoduplexes. The method involves generating
 CC homoduplexes and heteroduplexes in a sample and performing gel
 CC electrophoresis on the sample using a polyacrylamide gel that causes
 CC heteroduplexes to migrate more slowly than homoduplexes. The gel
 CC comprises 3-20% polyacrylamide, 1-50% of at least one denaturing agent
 CC selected from aliphatic alcohols, cyclic alcohols, allylic compounds,
 CC amides, ureas and carbamates, 10-100 mM borate-free TE [Tris-HCl, EDTA]
 CC buffer, and 10-100 mM taurine. The method has a high reliability and
 CC can be improved by allowing for the presence of the mutations in
 CC domains with high melting temperatures. These primers can specifically

CC detect a mutation in the human IVS17 3'-acceptor splice site.

SQ Sequence 19 BP; 8 A; 3 C; 6 G; 2 T; 0 other;
 Query Match 1.1%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 3.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 818 GCTGGAAATCCTCGA 832
 DB 1 GCTGGAAACCTCGA 15

RESULT 292

AAZ70613
 ID AAZ70613 standard; DNA; 19 BP.

XX AAZ70613;
 AC AAZ70613;
 XX 10-SEP-2001 (first entry)
 XX Human biallelic marker upstream amplification primer SEQ ID NO:4969.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.

OS WO954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-1800822.

XX 21-APR-1998; 98US-0082614.

XX 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium map of the human genome -

XX Claim 8; Page 1290; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the sequence listing from the present invention.

XX Sequence 19 BP; 2 A; 5 C; 2 G; 10 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 3.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1567 TTTTACTGTTTCTGA 1581
 DB 1 TTTTACTGTTTCTCA 15

RESULT 293

AAZ84233/C
 ID AAZ84233 standard; DNA; 19 BP.

XX AAZ84233;
 AC AAZ84233;

XX 04-DEC-2000 (first entry)

XX Cyclin C ribozyme binding site #205.

DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 XX restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US28772.

XX 04-DEC-1998; 98US-0110954.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1 -

XX Disclosure; Page 74; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAZ82415 to AAZ86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.

XX Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 other;

Query Match 1.1%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 3.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 913 TTTATTTCCTAAGTG 927
 DB 19 TTTATTTCCTAAGTG 5

RESULT 294

AAZ89251/C
 ID AAZ89251 standard; DNA; 19 BP.

XX AAZ89251;

XX 09-JUN-2000 (first entry)

XX Rat adenosine receptor 2a forward PCR primer.

XX Rat: expression profile; Three Prime End Amplification; TPEA;
 KW adenosine receptor 2a; PCR primer; ss.

XX OS Rattus sp.
XX AC WO200008208-A2.
XX DT 17-FEB-2000.
XX DE 05-AUG-1999; 99WO-GB02579.
XX KW 05-AUG-1998; 98GB-0017055.
XX KW (MEDI-) MEDICAL RES COUNCIL.
XX PI Freeman TC, Richardson PJ, Dixon AK;
XX DR WPI; 2000-224033/19.
XX Reverse transcription of mRNA species used for expression profiling of
PT single cells by employing a first heated primer to provide first strand
PT cDNA species and then a second heated primer population to generate
PT second strand cDNAs
XX Example 1; Page 30; 50pp; English.
XX This invention describes a novel process (M1) of reverse transcribing
CC mRNA species present in a sample from an organism by: (a) reverse
CC transcribing the mRNA species using a first heated primer, to provide a
CC first strand cDNA species; and (b) synthesizing second cDNA species
CC using a second heated primer population, the nucleotide sequences of the
CC non-heel portions of the second heated primers being such that the
CC reverse transcribed first strand cDNA species are capable of hybridizing
CC to at least one second primer. The processes can be used for hybridizing
CC profiling of single cells. The polynucleotide comprising an oligo d(T)
CC sequence and a heel sequence 5' can be used for the reverse
CC transcription of mRNA species in a sample. The polynucleotide primer
CC population of claim (4) can be used for the synthesis of second strand
CC cDNA from a population of first strand cDNA species. Single cell cDNA
CC libraries can be made for subsequent detailed analysis of gene expression
CC and the discovery of novel genes. Small samples can be used and allow
CC the utilization of the large amount of sequence data available for
CC further understanding of disease processes and the cellular physiology of
CC complex issues. The invention provides a rapid, robust and reproducible
CC procedure called Three Prime End Amplification (TPEA), optionally with
CC PCR (TPEA-PCR). Prior art methods for the analysis of gene expression
CC within single cells or small tissue samples are limiting. Whilst in situ
CC hybridization techniques provide detailed information about the
CC cellular expression pattern of a gene in intact tissue the technique is
CC laborious and unable to analyze multiple transcripts in a single
CC preparation. The methods presented in the disclosure provide a more
CC straightforward, reproducible and reliable cDNA amplification procedure
CC for small mRNA samples where expression profiling can be conducted. The
CC amplification technique can be carried out in a single tube with a need
CC for only limited manual intervention and large numbers of samples can
CC be analyzed. There is a bias towards more uniform length cDNA molecules
CC ensuring that even relatively low abundance mRNA species are transcribed
CC and optionally amplified at the same level of efficiency as more
CC abundant mRNA species. AAZ89191-289253 represent the primers described in
XX the method of the invention.

XX AH90994;
XX AC 09-OCT-2001 (first entry)
XX DE Human inflammatory bowel disease associated polymorphic site #59.
XX KW Human, inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT misc_feature 11
XX FT /*tag= a
XX FT /note= "SNP, optionally A or T at this position"
XX WO200142511-A2.
XX 14-JUN-2001.
XX 11-DEC-2000; 2000WO-US33632.
XX 10-DEC-1999; 99US-0170257.
XX 10-APR-2000; 2000US-0196046.
XX (WHEE) WHITEHEAD INST BIOMEDICAL RES.
XX (ELL1-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay -
XX Claim 1; Page 42; 463pp; English.
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention.
XX SQ Sequence 19 BP; 5 A; 0 C; 1 G; 12 T; 1 other;
Query Match 1.1%; Score 13.4; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1140 AAATTATTATTATTTT 1155
DQ ||||| |||||
4 AAATTATTATTATTTT 19
RESULT 296
AAH56758/c
ID AAH56758 standard; DNA; 19 BP.
XX AC AAH56758;
XX DT 06-SEP-2001 (first entry)
XX DE S. aureus groS operon antisense oligonucleotide SEQ ID NO:406.
XX KW Antisense oligonucleotide; groS; groEL; groES; inhibitor; growth;
XX KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
XX KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
XX KW antibacterial; antiviral; antiproliferative; antisense therapy;

XX SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1348 GCCAGCTCTGTGGT 1362
DQ ||||| |||||
19 GCCAGCTCTGTGGT 5
RESULT 295
AAH90994
ID AAH90994 standard; DNA; 19 BP.

KW microbial infection; ss.
XX
OS Staphylococcus aureus.
XX
PN WO200136625-A2.
XX
PD 25-MAY-2001.
XX
PP 20-NOV-2000; 2000WO-CA01347.
XX
PR 18-NOV-1999; 99US-0166249.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Dugourd D;
XX
DR WPI; 2001-355633/37.
XX
XX Novel antisense compounds targeting nucleic acid encoding groEL or
PT groES gene of microorganism, which hybridize with and inhibit
PT expression of the genes, useful to inhibit growth of microorganism
PT having the genes -
XX
XX
PS Claim 3; Page 52; 110pp; English.
XX
XX The present invention specifically claims AAH56368 to AAH56832 which are
CC antisense oligonucleotides to nucleotide sequences encoding groE. More
CC generally, antisense compounds (I) comprising antisense oligonucleotides
CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
CC shock protein (HSP)60 (GL) and groES (HSP10) (GS) gene from a
CC microorganism, where the antisense compound is complementary to GL or
CC GS of a microorganism and specifically hybridizes with and inhibits the
CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
CC and antiproliferative activities, and can be used in antisense therapy
CC and for inhibition of expression of groES or groEL. (I) are useful for
CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
CC also useful for inhibiting the growth of a microorganism, or inhibiting
CC the expression of GL or GS gene in a microorganism (a bacterial cell or
CC a virus) having a GL or GS gene which involves administering to the
CC microorganism or to a cell infected with the microorganism, (I). (I) are
CC also useful for treating a mammalian pathological condition mediated by
CC the microorganism which involves identifying a eukaryotic organism
CC having a pathological condition mediated by microorganisms having a GL
CC or GS gene and administering (I) such that the growth of microorganism
CC is inhibited. The antisense compounds are utilised for diagnostics,
CC therapeutic, prophylaxis and as research reagents and kits, e.g., to
CC prevent or delay microbial infections in humans. They are also useful as
CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
CC represent PCR primers for groE sequences which are used in the
CC exemplification of the present invention. AAH56855 to AAH56870 represent
CC groE nucleotide sequence given in the present invention.
XX
SQ Sequence 19 BP; 6 A; 1 C; 0 G; 12 T; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1591 AATATAAACTAAAT 1605
Db 15 AATATAAACTAAAT 1
RESULT 297
AAH59395/c
ID AAH59395 standard; DNA; 19 BP.
XX
AC AAH59395;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cyclin C ribozyme binding site SEQ ID NO:1819.
XX

KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; WWP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiskinning; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US29500.
XX
XX 26-OCT-1999; 99US-0161532.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Robbins JM, Tritz R;
XX
XX WPI; 2001-300427/31.
XX
XX Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX
XX Example 1; Page 204; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskinning,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 other;
Query Match 1.1%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 913 TTTATTTCTAAGTGG 927
Db 19 TTTATTTCTAAGTGG 5
RESULT 298
AAH57945/c
ID AAH57945 standard; DNA; 19 BP.
XX
AC AAH57945;
XX
XX 20-APR-2001 (first entry)
DT

XX Low abundance nucleic acid amplification PCR primer #16.
 XX Nucleic acid amplification; low abundance sequence; expression profiling;
 KW high throughput analysis; PCR primer; ss.
 XX Synthetic.
 XX WO200106004-A2.
 XX 25-JAN-2001.
 XX 19-JUL-2000; 2000WO-EP06887.
 XX 19-JUL-1999; 99US-0144666.
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES.
 XX Richardson P, Cox P;
 XX WPI; 2001-138470/14.
 XX Increasing the number of nucleotide sequences for low quantity mRNA
 PT species from a sample for detection and cloning of gene sequences -
 XX Example 1; Page 110; 120pp; English.
 XX The present invention describes methods of increasing the number of
 CC nucleic acid sequences corresponding to an mRNA present in a sample using
 CC heated primer sequences in amplification reactions. This is useful in the
 CC detection and cloning of low copy number mRNAs in a sample, in expression
 CC profiling and in high throughput systems.
 XX Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;
 SQ

Query Match 1.1%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. NO. 3.6e-02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1348 GCCAGCTGTGTGGT 1362
 |||||
 Db 19 GCCAGCTGTGTGGT 5

RESULT 299
 ABS97159
 ID ABS97159 standard; DNA; 19 BP.
 XX ABS97159;
 AC
 XX 23-DEC-2002 (first entry)
 XX Human CYP4501A2 Exon 3 PCR primer #2.
 XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
 KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxigenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW NNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase; thermolabile;
 KW STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactoferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological.
 XX Homo sapiens.
 OS

PN WO200257410-A2.
 XX 25-JUL-2002.
 XX 28-NOV-2001; 2001WO-US44838.
 XX 28-NOV-2000; 2000US-0724389.
 XX (DNAS-) DNA SCI LAB INC.
 XX Guida M, Hall J;
 XX WPI; 2002-698522/75.
 XX Isolated nucleic acid molecules having polymorphisms in known human
 PT genes e.g. cytochrome P450 and cathepsin S useful as genetic linkage
 PT markers for locating, identifying and characterizing the genes
 PT responsible for disorder-related traits -
 XX Example 2; Page 100; 714pp; English.
 XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxigenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase
 CC activating protein (FLAP), glutathione-S-transferase 12 (GST12),
 CC histamine-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC N-methyl transferase (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance
 CC 1 (MDR1), lactoferrin (LTF), multidrug resistance associated
 CC protein 3 (MRP3), orphan nuclear receptor (NR12), or acetylcholine
 CC muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or
 CC CHMR5) sequence. The polymorphisms in the human genes cited in the
 CC invention are useful as genetic linkage markers for locating and
 CC characterizing the genes that are responsible for specific traits within
 CC the genome and eventually identifying the genes responsible for a
 CC variety of disorder-related traits as a result of their e.g.,
 CC overexpression, constitutive expression, mutation or underexpression,
 CC which may be used in diagnosing and/or treating the disorders. The
 CC nucleic acid molecules comprising the polymorphic sequences contained
 CC in CYP4501A1, CYP4501A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2,
 CC NR12, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful
 CC for screening individuals for altered drug metabolism. The polymorphic
 CC sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may
 CC also be used to screen individuals for susceptibility to cancer.
 CC Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered
 CC cardiovascular function, in DBI or CHMR1 for altered central nervous system
 CC function, in FLAP and NNMT for altered pulmonary, immunological or
 CC haematological function, in KLK2 for altered serine protease activity in
 CC the prostate, in LTF for altered immunological or haematological
 CC function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral
 CC nervous system function. The present sequence represents a PCR
 CC primer used to amplify the sequences of the invention.
 XX Sequence 19 BP; 3 A; 1 C; 8 G; 7 T; 0 other;
 SQ

Query Match 1.1%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. NO. 3.6e-02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 482 TCTGTGTAGGGTTG 496
 |||||
 Db 2 TCTGTGTAGGGTTG 16

RESULT 300
 AAL45792/c

[illegible]

[illegible]

```
SQ Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 other;
Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1590 AAATATAAAGTAATAT 1607
Db 1 AAAATATAAATAATAT 18

RESULT 305
AAQ30302
ID AAQ30302 standard; DNA; 18 BP.
AC AAQ30302;
XX
XX
XX 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer HSV702 for forming triplex with HSV target duplex.
XX
KW Herpes simplex virus; I; AIDS; modified; HIV; RSV; HPV; malignancy;
KW hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 2 /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 3 /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 7 /tag= d
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 8 /tag= e
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 12 /tag= f
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 14 /tag= g
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 15 /tag= h
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US08811.
XX
XX 23-NOV-1990; 90US-0617907.
XX 18-JAN-1991; 91US-0643382.
XX 08-APR-1991; 91US-0683420.
XX 17-APR-1991; 91US-0686544.
XX 17-APR-1991; 91US-0686546.
XX 17-APR-1991; 91US-0686547.

PR 27-SEP-1991; 91US-0766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
XX hepatitis, herpes, malignancy and inflammation
XX
XX Claim 12; Page 67; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at
XX physiological pH with a purine rich target sequence by coupling
XX into the major groove of the duplex. The specific target sequence
XX of this oligomer is a herpes simplex virus 1 target duplex
XX beginning at nucleotide 52916 contg. a purine-rich region
XX concentrated on one chain of the duplex. The oligomer, and others
XX like it are useful in diagnosis and therapy of diseases characterised
XX by specific DNA duplex targets, e.g. respiratory syncytial virus, HIV,
XX hepatitis, herpes, malignant tumours and inflammation. The triple
XX helices form under mild conditions thus assays may be carried out
XX without subjecting the test specimen to harsh conditions. The oligomer
XX may contain an inverted polarity region formed from an o-xyloso
XX dimer synthon. The linking gp. is o-xyloso (nucleotides have the 3'
XX positions of xylose sugars linked via the o-xyloso ring). Two
XX nucleotides are coupled through a xyloso residue to form the dimer
XX synthon. This additional modification may render the oligomer stable
XX to nuclease activity. The oligomer is able to inhibit gene expression,
XX as verified by in vitro systems.
XX See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 8 A; 0 C; 0 G; 10 T; 0 other;
Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1611 ACATTAAATATAATTT 1628
Db 1 AAATTTAATTATAATTT 18

RESULT 306
AAQ30368
ID AAQ30368 standard; DNA; 18 BP.
AC AAQ30368;
XX
XX 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
XX Oligomer HUM beta 102 for forming triplex with IL-1 target duplex.
XX Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
XX HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 2 /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 7 /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 10 /tag= c
```

FT	/mod_base= OTHER
FT	/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	12
FT	modified_base
FT	/*tag= d
FT	/mod_base= OTHER
FT	/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	14
FT	modified_base
FT	/*tag= e
FT	/mod_base= OTHER
FT	/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	13..18
FT	misc_feature
FT	/*tag= f
FT	/label= inverted_polarity_region
FT	/note= "see comments"
FT	12..13
FT	misc_feature
FT	/*tag= g
FT	/note= "O-xylosa dimer synthon linkage"
XX	
PN	MO9209705-AI.
XX	
PD	11-JUN-1992.
XX	
PP	25-NOV-1991; 91WO-US08811.
XX	
PR	23-NOV-1990; 90US-0617907.
PR	18-JAN-1991; 91US-0643382.
PR	08-APR-1991; 91US-0683420.
PR	17-APR-1991; 91US-0686544.
PR	17-APR-1991; 91US-0686546.
PR	17-APR-1991; 91US-0686547.
PR	27-SEP-1991; 91US-0766733.
XX	
PA	(GILB-) GILEAD SCI INC.
PI	Proehler B, Krawczyk S, Matteucci MD, Milligan J;
XX	
DR	WPI; 1992-217083/26.
XX	
PT	New oligomers contg. modified bases - which form a triplex with
PT	G-C doublet in a DNA duplex, for treating and diagnosing HIV,
PT	hepatitis, herpes, malignancy and inflammation
XX	
PS	Claim 12; Page 69; 77pp; English.
XX	
CC	The synthetic oligomer is capable of forming a triplex at
CC	physiological pH with a purine rich target sequence by coupling
CC	into the major groove of the duplex. The specific target sequence
CC	of this oligomer is the human interleukin -1 beta gene beginning at
CC	nucleotide 8379 contg. a purine rich sequence concd. on one strand
CC	of the duplex. The oligomer, and others like it are useful in
CC	diagnosis and therapy of diseases characterised by specific DNA
CC	duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant
CC	tumours and inflammation. The triple helices form under mild conditions
CC	thus assays may be carried out without subjecting the test specimen to
CC	harsh conditions. The oligomer contains an inverted polarity region to
CC	formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
CC	(nucleotides have the 3' positions of xylose sugars linked via the
CC	o-xylyene ring). Two nucleotides are coupled through a xylene residue
CC	to form the dimer synthon. This additional modifications may render
CC	the oligomer stable to nuclease activity. The oligomer is able to
CC	inhibit gene expression, as verified by in vitro systems.
CC	See also AAQ25452-25501 and AAQ30226-448.
CC	(updated on 25-MAR-2003 to correct EN field.)
XX	
SQ	Sequence 18 BP; 5 A; 0 C; 0 G; 13 T; 0 other;

RESULT 307	AAV14091	AAV14091 standard; DNA; 18 BP.
ID	AAV14091	
AC	AAV14091;	
CC		
XX		
DT	19-MAY-1998 (first entry)	
XX		
DE	Probe HBPr257 for RT pol region	
XX		
KW	Probe; hepatitis b virus; HBV det	
KM	preCore region; HBsAg region; ge	
KW	mutation detection; ss.	
XX		
CS	Synthetic.	
OS	Hepatitis b virus.	
XX		
PN	WO9740193-A2.	
PD	30-OCT-1997.	
XX		
PF	21-APR-1997; 97WO-BP02002.	
XX		
PR	19-APR-1996; 96EP-0870053.	
PA	(INNO-) INNOGENETICS NV.	
PI	Maertens G, Rossau R, Stuyver	
XX	WPI; 1997-535867/49.	
DR		
XX		
PT	Detection and/or genetic analysis	
PT	specifically genotype, preCore m	
PT	and RT gene mutations selected b	
XX		
FS	Claim 5; Page 32; 80pp; English.	
CC		
CC	This sequence represents a probe	
CC	b virus (HBV). This sequence can	
CC	for detection and/or genetic anal	
CC	sample. The method comprises: (a	
CC	concentrating polynucleic acids	
CC	relevant part of a suitable HBV	
CC	suitable primer pair; (b) hybrid	
CC	2 nucleotide probes, which are a	
CC	support and hybridise specific	
CC	the HBV RT pol gene region, HBV	
CC	genotype specific target sequenc	
CC	homologues; (c) detecting the hy	
CC	the HBV genotype and/or mutants	
CC	differential hybridisation signal	
CC	diagnose and/or monitor HBV muta	
CC	specifically genotype, preCore m	
CC	RT gene mutations selected by tr	
CC	pencilciovir.	
XX		
XX		
SQ	Sequence 18 BP; 7 A; 0 C; 4 G; 7	
	Query Match 1.1%; Sco	
	Best Local Similarity 83.3%; Pre	
	Matches 15; Conservative 0;	
Qy	1123 TATAAGATGTTATAGTA 1140	
Db	1 TATGATGATGATATAGTA 18	
RESULT 308	AAV14083	AAV14083 standard; DNA; 18 BP.
ID	AAV14083	
XX		

```

Query Match      1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1123  TATAAGAGCTTATAGTA 1140
          |||  ||||| |||||
Db      1  TATGTAGATGATATAGTA 18

RESULT 308
AAVL4083
ID      AAVL4083 standard; DNA; 18 BP.
XX

```


AAV14083;
19-MAY-1998 (first entry)
Probe HBP249 for RT pol region of HBV.
Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
preCore region; HBsAg region; genotype specific target;
mutation detection; ss.
Synthetic.
Hepatitis b virus.
WO9740193-A2.
30-OCT-1997.
21-APR-1997; 97WO-EP02002.
19-APR-1996; 96EP-0870053.
(INNO-) INNOGENETICS NV.
Maertens G, Rossau R, Stuyver L;
WPI; 1997-535867/49.
Detection and/or genetic analysis of hepatitis B virus -
specifically genotype, preCore mutations, vaccine escape mutations
and RT gene mutations selected by treatment with drugs
Claim 5; Page 32; 80pp; English.
This sequence represents a probe for the RT pol region of hepatitis
b virus (HBV). This sequence can be used in the method of the invention
for detection and/or genetic analysis of hepatitis B virus (HBV) in a
sample. The method comprises: (a) optionally releasing, isolating or
concentrating polynucleic acids (I) in the sample, and amplifying the
relevant part of a suitable HBV gene in the sample with at least 1
suitable primer pair; (b) hybridising (I) with a combination of at least
2 nucleotide probes, which are applied to known locations on a solid
support and hybridise specifically to mutant target sequences chosen from
the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
genotype specific target sequences, or their complements or U for T
homologues; (c) detecting the hybrids formed in step (b), and inferring
the HBV genotype and/or mutants present in the sample from the
differential hybridisation signal(s). The composition can be used to
diagnose and/or monitor HBV mutants and/or genotypes in a sample,
specifically genotype, preCore mutations, vaccine escape mutations and
RT gene mutations selected by treatment with drugs, e.g. lamivudine and
penciclovir.
Sequence 18 BP; 7 A; 0 C; 4 G; 7 T; 0 other;
Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1123 TATAAGACATGTTATAGTA 1140
Dy 1 TATATGATGATATAGTA 18
RESULT 309
AAV14088
ID AAV14088 standard; DNA; 18 BP.
AC AAV14088;
19-MAY-1998 (first entry)
Probe HBP254 for RT pol region of HBV.

AAV14083;
19-MAY-1998 (first entry)
Probe HBP249 for RT pol region of HBV.
Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
preCore region; HBsAg region; genotype specific target;
mutation detection; ss.
Synthetic.
Hepatitis b virus.
WO9740193-A2.
30-OCT-1997.
21-APR-1997; 97WO-EP02002.
19-APR-1996; 96EP-0870053.
(INNO-) INNOGENETICS NV.
Maertens G, Rossau R, Stuyver L;
WPI; 1997-535867/49.
Detection and/or genetic analysis of hepatitis B virus -
specifically genotype, preCore mutations, vaccine escape mutations
and RT gene mutations selected by treatment with drugs
Claim 5; Page 32; 80pp; English.
This sequence represents a probe for the RT pol region of hepatitis
b virus (HBV). This sequence can be used in the method of the invention
for detection and/or genetic analysis of hepatitis B virus (HBV) in a
sample. The method comprises: (a) optionally releasing, isolating or
concentrating polynucleic acids (I) in the sample, and amplifying the
relevant part of a suitable HBV gene in the sample with at least 1
suitable primer pair; (b) hybridising (I) with a combination of at least
2 nucleotide probes, which are applied to known locations on a solid
support and hybridise specifically to mutant target sequences chosen from
the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
genotype specific target sequences, or their complements or U for T
homologues; (c) detecting the hybrids formed in step (b), and inferring
the HBV genotype and/or mutants present in the sample from the
differential hybridisation signal(s). The composition can be used to
diagnose and/or monitor HBV mutants and/or genotypes in a sample,
specifically genotype, preCore mutations, vaccine escape mutations and
RT gene mutations selected by treatment with drugs, e.g. lamivudine and
penciclovir.
Sequence 18 BP; 7 A; 1 C; 3 G; 7 T; 0 other;
Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1123 TATAAGACATGTTATAGTA 1140
Dy 1 TATATGATGATATAGTA 18
RESULT 310
AAV14089
ID AAV14089 standard; DNA; 18 BP.
AC AAV14089;
19-MAY-1998 (first entry)
Probe HBP255 for RT pol region of HBV.
Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
preCore region; HBsAg region; genotype specific target;
mutation detection; ss.
Synthetic.
Hepatitis b virus.

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XX PN WO9740193-A2.
XX PD 30-OCT-1997.
XX PF 21-APR-1997; 97WO-EP02002.
XX PR 19-APR-1996; 96EP-0870053.
XX PA (INNO-) INNOGENETICS NV.
XX PI Maartens G, Rossau R, Stuyver L;
XX DR WPI; 1997-535867/49.
XX PT Detection and/or genetic analysis of hepatitis B virus -
XX PT specifically genotype, preCore mutations, vaccine escape mutations
XX PT and RT gene mutations selected by treatment with drugs
XX PS Claim 5; Page 32; 80pp; English.
XX CC This sequence represents a probe for the RT pol region of hepatitis
XX CC b virus (HBV). This sequence can be used in the method of the invention
XX CC for detection and/or genetic analysis of hepatitis B virus (HBV) in a
XX CC sample. The method comprises: (a) optionally releasing, isolating or
XX CC concentrating polynucleic acids (I) in the sample, and amplifying the
XX CC relevant part of a suitable HBV gene in the sample with at least 1
XX CC suitable primer pair; (b) hybridising (I) with a combination of at least
XX CC 2 nucleotide probes, which are applied to known locations on a solid
XX CC support and hybridise specifically to mutant target sequences chosen from
XX CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
XX CC genotype specific target sequences, or their complements or U for T
XX CC homologues; (c) detecting the hybrids formed in step (b), and inferring
XX CC the HBV genotype and/or mutants present in the sample from the
XX CC differential hybridisation signal(s). The composition can be used to
XX CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
XX CC specifically genotype, preCore mutations, vaccine escape mutations and
XX CC RT gene mutations selected by treatment with drugs, e.g. lamivudine and
XX CC penciclovir.
XX SQ Sequence 18 BP; 7 A; 0 C; 3 G; 8 T; 0 other;

  Query Match 1.1%; Score 13.2; DB 1; Length 18;
  Best Local Similarity 83.3%; Pred. No. 3.8e+02;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1123 TATATGATGATATAGTA 1140
Db 1 TATATGATGATATAGTA 18

RESULT 311
AAT68917
XX ID AAT68917 standard; DNA; 18 BP.
XX AC AAT68917;
XX AT AAT68917;
XX DT 04-FEB-1998 (first entry)
XX DE Sense primer 1 for eNOS gene 5'-flanking region (-786).
XX KW 5'-flanking region; PCR primer; analysis;
XX KW endothelial nitrogen monoxide synthase; eNOS; genetic screening;
XX KW coronary arterial spasm; angina pectoris; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9718327-A1.
XX PD 22-MAY-1997.
XX PF 13-NOV-1996; 96WO-JP03324.

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XX PR 28-JUN-1996; 96JP-0168761.
XX PR 13-NOV-1995; 95JP-0319504.
XX PA (SHIO) SHIONOGI & CO LTD.
XX PI Yasue H, Yoshimura M;
XX DR WPI; 1997-289303/26.
XX PT Genetic screening for diseases associated with coronary arterial
XX PT spasm - by assessment of the occurrence of specific mutation(s) of
XX PT the endothelial nitrogen monoxide synthase gene
XX PS Example 7; Page 26; 47pp; Japanese.
XX CC The present sequence is a primer for the PCR amplification of the
XX CC endothelial nitrogen monoxide synthase (eNOS) gene 5'-flanking
XX CC region (-1468). The amplification product was used in an example of
XX CC genetic screening method for diseases associated with coronary
XX CC arterial spasm, which comprises determining if 1 or more specific
XX CC nucleotides in the eNOS gene have been substituted, specifically
XX CC G894T, C774T, T(-786)C, A(-922)G and T(-1468)A. Screening for
XX CC diseases associated with coronary spasm, e.g. angina pectoris,
XX CC cannot be easily carried out by existing methods, this method
XX CC allows rapid and easy detection.
XX SQ Sequence 18 BP; 1 A; 1 C; 7 G; 9 T; 0 other;

  Query Match 1.1%; Score 13.2; DB 1; Length 18;
  Best Local Similarity 83.3%; Pred. No. 3.8e+02;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1355 GTGTTGCTAGTCTGTGT 1372
Db 1 GGGTTGTAGTCTGTGT 18

RESULT 312
AAV36356/C
XX ID AAV36356 standard; DNA; 18 BP.
XX AC AAV36356;
XX DT 10-NOV-1998 (first entry)
XX DE Antisense oligonucleotide HADA3MM1, targeting adenosine A3 receptor.
XX KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;
XX KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;
XX KW allergy; emphysema; cystic fibrosis; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "contains phosphorothioate internucleotide
XX PN WO9823294-A1.
XX PD 04-JUN-1998.
XX PF 26-NOV-1997; 97WO-US22017.
XX PR 26-NOV-1996; 96US-0757024.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX

```

DR WPI; 1998-322464/28.

XX Treating respiratory disease with antisense sequences directed

PT against adenosine or bradykinin receptors - with localised delivery

PT to the respiratory system, suitable for long term treatment of

PT asthma, adult respiratory distress syndrome etc.

XX

PS Example 1; Page 30; 47pp; English.

XX

CC Sequences AAV36356 and AAV36358 are anti-sense oligonucleotides used as

CC mismatched controls to target the human adenosine A3 receptor and thus

CC test the other oligonucleotides, AAV36355 and AAV36357 respectively, the

CC design of which required the secondary structure of the targeted mRNA.

CC The adenosine receptor mRNA secondary structure was both analysed and

CC used to construct antisense oligonucleotides containing a

CC phosphorothioate backbone. Once the antisense molecules are created

CC they can be used to target their predetermined sequence, thus causing the

CC gene product to decrease. The antisense oligonucleotides were targeted

CC to specific mRNA regions containing either a junction between the intron

CC and exon, or where they may overlap the initiation codon. The receptor

CC is a member of the G-protein coupled family of cell surface receptors

CC that have 7-transmembrane segments. These oligonucleotides can be used

CC to treat or prevent conditions associated with bronchoconstriction

CC and/or lung inflammation in humans or other animals e.g. asthma,

CC pulmonary disease, allergy, emphysema and cystic fibrosis.

XX

SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 869 GCCAGGATCCCAAGTCC 886

Db 18 GCCATGATCCGCAAGTAC 1

RESULT 313

AAAX90242

ID AAAX90242 standard; DNA; 18 BP.

AC AAAX90242;

XX

DT 23-SEP-1999 (first entry)

XX

DE GRK4 allele specific probe #9.

XX

KW Human; antibody; G-protein-related kinase; GRK4; mutant; hypertension;

KW probe; ss.

OS Synthetic.

OS Homo sapiens.

XX

PN W09935279-A1.

XX

PD 15-JUL-1999.

XX

PF 12-JAN-1999; 99WO-US00663.

XX

PR 28-AUG-1998; 98US-0098279.

XX

PR 12-JAN-1998; 98US-0071199.

XX

XX (G80U) UNIV GEORGETOWN MEDICAL CENT.

FA (UVVI-) UNIV VIRGINIA PATENT FOUND.

XX

PI Felder R, Jose P;

XX

DR WPI; 1999-444199/37.

XX

XX G protein-coupled receptor kinase 4 mutants associated with

PT essential hypertension, useful for identifying anti-hypertensive

PT drugs

XX

PS Disclosure; Page 20; 54pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule

CC encoding a G protein-coupled receptor kinase (GRK) 4 protein having an

CC R65L, A142V or R65L, R486 double mutation or an R65L, A142V, R486V

CC triple mutation. A transgenic animal, comprising a diploid genome in

CC comprising a transgene encoding a GRK4 protein which is expressed in

CC renal cells to produce the GRK4 protein, and where expression of the

CC transgene causes the transgenic animal to exhibit a state of essential

CC hypertension compared to a normotensive animal whose renal cells do not

CC express the GRK4 protein. The transgenic animal, especially a mouse, is

CC useful as a model for essential hypertension. The transgenic animal's

CC renal cells have a decreased ability to reject sodium compared to a

CC normotensive animal whose renal cells do not express GRK4. The animal

CC model, and reconstituted whole cell system, can be used to identify

CC putative anti-hypertensive agents. The GRK4 protein complex and

CC immortalized kidney cell cultures can also be used to identify putative

CC anti-hypertensive agents. Drugs, e.g. antisense GRK4 RNA, a GRK4

CC ribozyme or a GRK4 dominant negative mutant DNA molecule, that interact

CC with GRK4 can be used to increase natriuresis (decrease sodium

CC transport) in essential hypertensive individuals. The present sequence

CC represents a GRK4 allele specific probe from the present invention.

XX

SQ Sequence 18 BP; 3 A; 3 C; 6 G; 6 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 484 TGTGTAGGCTTCCGACA 501

Db 1 TGTGTAGGCTTCCGCTGA 18

RESULT 314

AAAX57900

ID AAAX57900 standard; DNA; 18 BP.

XX

AC AAAX57900;

XX

DT 15-JUL-1999 (first entry)

XX

DE PCR primer for construction of Acma derivatives.

XX

KW Acma repeat; consensus sequence; major peptidoglycan hydrolase; vaccine;

KW cell wall attachment; substance delivery; diagnosis; bioadsorption;

KW PCR primer; ss.

XX

OS Synthetic.

XX

XX RP916726-A1.

XX

PD 19-MAY-1999.

XX

PF 13-NOV-1997; 97EP-0203539.

XX

PR 13-NOV-1997; 97EP-0203539.

XX

PA (UWGR-) RIJKSUNIV GROWINGEN.

XX

DR WPI; 1999-290024/25.

XX

PT New proteinaceous substance comprising a sequence consensus to a

PT major peptidoglycan (Acma), useful for attaching a substance to a

PT cell wall

XX

PS Example; Page 18; 98pp; English.

XX

CC This sequence represents a PCR primer used in the construction of

CC acma derivatives. The invention relates to

CC a proteinaceous substance that comprises at least one stretch

CC of amino acids derived from a first organism, capable of attaching

CC to a cell wall of a second microorganism. The proteinaceous

CC substance is useful in a method for attaching a substance to the cell
 CC wall of a microorganism, and the substance and either microorganism are
 CC used in pharmaceutical compositions and vaccines, for delivery of a
 CC substance to a cell. They are also useful in diagnostic tests,
 CC bioadsorption processes and in foodstuffs. The new method targets
 CC substances to cells of a wide range of microorganisms, unlike prior art
 CC anchoring and targeting proteins which are specific and selective for a
 CC limited set of microorganisms, which are usually recombinant or
 CC pathogenic. The second microorganism in the new method is
 CC non-recombinant, preventing restrictions on applications, and preventing
 CC potential problems of colonisation of the mucosal surfaces which
 CC generates long term exposure to the target antigens expressed, which can
 CC cause immune tolerance. Public consensus is against use of recombinant or
 CC attenuated strains, so the new technique is more likely to be accepted
 CC than prior art methods.

XX
 SQ Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1313 AACAACTCCTAGTTTGATA 1330
 ||||| ||||| ||||| |||||
 Db 1 AGCAATACCTAGTTTATA 18

RESULT 315
 AAX28308
 ID AAX28308 standard; DNA; 18 BP.
 AC AAX28308;
 XX
 XX 17-JUN-1999 (first entry)
 DE
 DE PCR primer for Human CYP3A4 gene promoter.

CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
 CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
 genetic linkage detection; phenotypic variation; promoter; PCR primer;
 ss.

OS Synthetic.
 OS Homo sapiens.
 XX WO9913106-A1.
 XX 18-MAR-1999.
 PD
 XX 02-SEP-1998; 98WO-US18158.
 XX 10-SEP-1997; 97US-0058612.
 XX (AXYS-) AXYS PHARM INC.

XX Guida M, Lichter JB;
 XX WPI; 1999-215070/18.
 XX New isolated CYP3A4 polymorphic sequences
 XX Example; Page 18; 40pp; English.

XX This sequence represents a PCR primer for the human CYP3A4 gene promoter.
 CC The invention relates to a CYP3A4 sequence polymorphism,
 CC which is part of a non-naturally occurring chromosome. Nucleic acids
 CC comprising the CYP3A4 polymorphic sequences can be used to screen
 CC patients for altered metabolism for CYP3A4 substrates, potential
 CC drug-drug interactions, and adverse/side effects as well as diseases that
 CC result from environmental or occupational exposure to toxins. They can
 CC also be used to establish animal, cell culture and in vitro cell-free
 CC models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used
 CC for expression studies to determine the effect of promoter and/or intron

CC sequence variations on mRNA expression and stability. The polymorphisms
 CC are also used as single nucleotide polymorphisms to detect genetic
 CC linkage to phenotypic variation in activity and expression of CYP3A4. The
 CC nucleic acids can also be used to generate genetically modified non-human
 CC animals or site specific gene modifications in cell lines.

XX Sequence 18 BP; 10 A; 2 C; 6 G; 0 U; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 414 CAAGAATCAGTGAACATG 431
 ||||| ||||| ||||| |||||
 Db 1 CARGAACHGAGAGAGG 18

RESULT 316
 AAZ71080/c
 ID AAZ71080 standard; DNA; 18 BP.

AC AAZ71080;

XX 10-SEP-2001 (first entry)

Human biallelic marker upstream amplification primer SEQ ID NO:5436.

XX Human genome; biallelic marker; high density disequilibrium map;
 XX Genomic map; haplotype; phenotype; polymorphic base; genotyping;
 XX haplotyping; hybridisation; identification; characterisation;
 XX amplification; single nucleotide polymorphism; SNP; PCR primer;
 XX diagnosis; ss.

OS Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB00822.

XX 21-APR-1998; 98US-0082614.

XX 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome -

XX Claim 8; Page 1390; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.

XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.

XX Sequence 18 BP; 5 A; 6 C; 2 G; 5 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 421 CAGTGAAGATCCAGTGA 438
 |||||
 Db 18 CAGTGAAGGTCTCAGTTA 1

RESULT 317

AAZ40682/c
 ID AAZ40682 standard; RNA; 18 BP.

XX AAZ40682;

DT 17-MAR-2000 (first entry)

DE Yersinia YopE mRNA fragment.

KW Type III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;

KW macrophage; antisense; ss.

OS Yersinia enterocolitica.

PN WO9960011-A1.

PD 25-NOV-1999.

PF 21-MAY-1999; 99WO-US11361.

PR 21-MAY-1998; 98US-0086302.

PA (REGC) UNIV CALIFORNIA.

PI Schneewind O, Anderson DM;

DR WPI; 2000-072427/06.

PT Antisense oligonucleotide inhibition useful for suppression of
 virulence and improvement of host defense mechanisms such as
 phagocytosis -

PS Disclosure; Page 28; 50pp; English.

CC The invention relates to a method of inhibiting Type III secretion of
 proteins by Yersinia by contacting the cell with an antisense oligo that
 binds at least a portion of mRNA encoding the first 15 amino acids of
 either the wild-type YopE or YopN protein. The methods are useful for
 inhibiting Type III secretion of proteins by Yersinia (especially Yop
 proteins which allow Yersinia to evade phagocytic killing by macrophages)
 and other Gram-negative bacteria, where the antisense oligonucleotide
 binds a portion of mRNA encoding a secretion signal of a secreted protein
 of a Gram-negative bacterium. The Gram-negative bacterium that can be
 targeted include Yersinia spp., Escherichia coli, Salmonella spp.,
 Shigella spp., Pseudomonas spp. and Xanthomonas spp. Inhibiting Type III
 secretion of proteins is useful for enhancing a hosts defenses against
 such bacteria. The methods also provide a means for screening for
 compounds, which block or inhibit the type III secretion.

XX Sequence 18 BP; 9 A; 2 C; 0 G; 7 U; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1160 ATTAATGATGCTTTATT 1177
 |||||
 Db 18 ATTAATGATGATTTT 1

RESULT 318

AAZ40683/c

ID AAZ40683 standard; RNA; 18 BP.

XX AAZ40683;

DT 17-MAR-2000 (first entry)

DE Yersinia YopE spontaneous suppressor mutant fragment.

KW Type III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;

KW macrophage; antisense; ss.

OS Yersinia enterocolitica.

PN WO9960011-A1.

PD 25-NOV-1999.

PF 21-MAY-1999; 99WO-US11361.

PR 21-MAY-1998; 98US-0086302.

PA (REGC) UNIV CALIFORNIA.

PI Schneewind O, Anderson DM;

DR WPI; 2000-072427/06.

PT Antisense oligonucleotide inhibition useful for suppression of
 virulence and improvement of host defense mechanisms such as
 phagocytosis -

PS Disclosure; Page 28; 50pp; English.

CC The invention relates to a method of inhibiting Type III secretion of
 proteins by Yersinia by contacting the cell with an antisense oligo that
 binds at least a portion of mRNA encoding the first 15 amino acids of
 either the wild-type YopE or YopN protein. The methods are useful for
 inhibiting Type III secretion of proteins by Yersinia (especially Yop
 proteins which allow Yersinia to evade phagocytic killing by macrophages)
 and other Gram-negative bacteria, where the antisense oligonucleotide
 binds a portion of mRNA encoding a secretion signal of a secreted protein
 of a Gram-negative bacterium. The Gram-negative bacterium that can be
 targeted include Yersinia spp., Escherichia coli, Salmonella spp.,
 Shigella spp., Pseudomonas spp. and Xanthomonas spp. Inhibiting Type III
 secretion of proteins is useful for enhancing a hosts defenses against
 such bacteria. The methods also provide a means for screening for
 compounds, which block or inhibit the type III secretion.

XX Sequence 18 BP; 9 A; 2 C; 1 G; 6 U; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1160 ATTAATGATGCTTTATT 1177
 |||||
 Db 18 ATTAATGATGCTTTATT 1

RESULT 319

AAZ40684/c

ID AAZ40684 standard; RNA; 18 BP.

XX AAZ40684;

DT 17-MAR-2000 (first entry)

DE Yersinia YopE spontaneous suppressor mutant fragment.

KW Type III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;

KW macrophage; antisense; ss.

OS Yersinia enterocolitica.
 OS Synthetic.
 PN WO9960011-AL.
 XX
 XX 25-NOV-1999.
 XX
 XX 21-MAY-1999; 99MO-US11361.
 XX
 XX 21-MAY-1998; 98US-0086302.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Schneewind O, Anderson DM;
 PI
 DR WPI; 2000-072427/06.
 XX
 XX Antisense oligonucleotide inhibition useful for suppression of
 PT virulence and improvement of host defense mechanisms such as
 PT phagocytosis -
 XX
 XX Disclosure; Page 28; 50pp; English.
 XX
 XX The invention relates to a method of inhibiting Type III secretion of
 CC proteins by Yersinia by contacting the cell with an antisense oligo that
 CC binds at least a portion of mRNA encoding the first 15 amino acids of
 CC either the wild-type YopE or YopN protein. The methods are useful for
 CC inhibiting Type III secretion of proteins by Yersinia (especially Yop
 CC proteins which allow Yersinia to evade phagocytic killing by macrophages)
 CC and other Gram-negative bacteria, where the antisense oligonucleotide
 CC binds a portion of mRNA encoding a secretion signal of a secreted protein
 CC of a Gram-negative bacterium. The Gram-negative bacterium that can be
 CC targeted include Yersinia spp., Escherichia coli, Salmonella spp.,
 CC Shigella spp., Pseudomonas spp. and Xanthomonas spp. Inhibiting Type III
 CC secretion of proteins is useful for enhancing a hosts defenses against
 CC such bacteria. The methods also provide a means for screening for
 CC compounds, which block or inhibit the type III secretion.
 XX
 XX Sequence 18 BP; 9 A; 2 C; 1 G; 6 U; 0 other;
 SQ
 Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1160 ATTAATGATGCTTTTATT 1177
 Db 18 ATTAATGATGCTTTTATT 1
 |||||
 RESULT 320
 AA240685/C
 ID AA240685 standard; RNA; 18 BP.
 XX
 XX AA240685;
 AC
 DT 17-MAR-2000 (first entry)
 XX
 XX Yersinia YopE spontaneous suppressor mutant fragment.
 DE
 XX Type III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;
 KW macrophage; antisense; ss.
 XX
 XX Yersinia enterocolitica.
 OS Synthetic.
 XX
 XX WO9960011-AL.
 PN
 XX 25-NOV-1999.
 XX
 XX 21-MAY-1999; 99MO-US11361.
 XX
 XX 21-MAY-1998; 98US-0086302.
 XX

PA (REGC) UNIV CALIFORNIA.
 XX
 XX Schneewind O, Anderson DM;
 XI
 DR WPI; 2000-072427/06.
 XX
 XX Antisense oligonucleotide inhibition useful for suppression of
 PT virulence and improvement of host defense mechanisms such as
 PT phagocytosis -
 XX
 XX Disclosure; Page 28; 50pp; English.
 XX
 XX The invention relates to a method of inhibiting Type III secretion of
 CC proteins by Yersinia by contacting the cell with an antisense oligo that
 CC binds at least a portion of mRNA encoding the first 15 amino acids of
 CC either the wild-type YopE or YopN protein. The methods are useful for
 CC inhibiting Type III secretion of proteins by Yersinia (especially Yop
 CC proteins which allow Yersinia to evade phagocytic killing by macrophages)
 CC and other Gram-negative bacteria, where the antisense oligonucleotide
 CC binds a portion of mRNA encoding a secretion signal of a secreted protein
 CC of a Gram-negative bacterium. The Gram-negative bacterium that can be
 CC targeted include Yersinia spp., Escherichia coli, Salmonella spp.,
 CC Shigella spp., Pseudomonas spp. and Xanthomonas spp. Inhibiting Type III
 CC secretion of proteins is useful for enhancing a hosts defenses against
 CC such bacteria. The methods also provide a means for screening for
 CC compounds, which block or inhibit the type III secretion.
 XX
 XX Sequence 18 BP; 9 A; 2 C; 0 G; 7 U; 0 other;
 SQ
 Query Match 1.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1160 ATTAATGATGCTTTTATT 1177
 Db 18 ATTAATGATGCTTTTATT 1
 |||||
 RESULT 321
 AA217638/C
 ID AAD17638 standard; DNA; 18 BP.
 XX
 XX AAD17638;
 AC AAD17638;
 DT 10-DEC-2001 (first entry)
 XX
 XX Human GCPII gene exon-4 amplifying PCR primer #1.
 DE
 XX Human; glutamate carboxypeptidase II; GCPII gene; dietary folate; FGCP;
 KW folypoly-gamma-glutamate carboxypeptidase; hyperhomocysteinaemia;
 KW cardiovascular disease; Alzheimer's disease; neural tube defect;
 KW congenital heart defect; colon cancer; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200168897-A2.
 PN
 XX 20-SEP-2001.
 PD
 XX 12-MAR-2001; 2001WO-US07880.
 XX
 XX 13-MAR-2000; 2000US-0188983.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Halsted CH, Devlin AM;
 PI
 XX WPI; 2001-582462/65.
 DR
 XX Screening an individual for increased risk of low folate status,
 PT comprises detecting mutation in human glutamate carboxypeptidase II
 PT gene which affects ability of hydrolyzing terminal glutamates from
 PT dietary folates -

XX Example 5; Page 26; 38pp; English.

PS The patent discloses methods for screening an individual for increased

XX risk of low folate status. The method involves detecting a mutation

CC in the human glutamate carboxypeptidase (Gcp) II gene in a biological

CC sample from said individual, wherein detection of the mutation is

CC indicative of decreased ability of an individual to hydrolyse terminal

CC glutamate residues from dietary folates by folypoly-gamma-glutamate

CC carboxypeptidase (PCGP), a product of GCP II gene. The decreased ability

CC is associated with low folate status. The method is useful for screening

CC an individual for increased risk of low folate status and conditions

CC associated with hyperhomocysteinemia, cardiovascular disease, colon

CC cancer and altered cognition in the elderly including Alzheimer's

CC disease. Pregnant women with low folate status are at increased risk

CC of bearing children with neural tube defects and congenital heart

CC defects. The present DNA sequence is a PCR primer which is used for

CC amplifying exon-4 of GCP II gene. This primer is designed from PSMA

CC genomic sequence and is used for detecting a mutation in GCP II gene.

XX Sequence 18 BP; 7 A; 3 C; 2 G; 6 T; 0 other;

SQ Query Match 1.1%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1230 CAGTAAATTTTCATTC 1247

Db 18 CAGTAAAGTTGATTAC 1

RESULT 322

AAH26220/c

ID AAH26220 standard; DNA; 18 BP.

XX AAH26220;

XX 17-SEP-2001 (first entry)

XX Parathyroid hormone cDNA 3' PCR primer.

DE Parathyroid hormone; parathormone; PTH; kidney failure; rat;

KW osteoporosis; gene therapy; ss.

XX Rattus sp.

XX WO200149838-A2.

XX 12-JUL-2001.

XX 02-JAN-2001; 2001WO-IL00006.

XX 03-JAN-2000; 2000IL-0133875.

XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX Silver J, Naveh T;

XX WPI; 2001-432876/46.

XX Novel isolated cis-acting regulatory nucleic acid sequence comprising

PT 3'-untranslated region of parathyroid hormone gene useful in gene

PT therapy for treating pathological condition such as chronic renal

PT failure -

XX Example 1; Page 39; 83pp; English.

PS The present sequence is that of a 3' PCR primer used in the

CC amplification of a 40 nucleotide transcript, which was used in

CC the construction of a plasmid containing rat parathyroid

CC hormone (PTH) cDNA. Cis-acting sequences (see AAH26198-211)

CC comprising fragments of the 3' untranslated region of mammalian PTH

CC genes, or allelic variants, mutants or functionally equivalent

CC fragments, can be linked to a heterologous or homologous coding

CC sequence of interest, and direct specific regulation of stability of

CC the mRNA encoded by the linked coding sequence. The regulation of

CC the stability of the mRNA is responsive to changes in serum levels

CC of any one of calcium and phosphate and is further mediated by the

CC binding of at least one parathyroid protein or its derivatives to

CC the cis-acting sequence. A pharmaceutical composition for

CC prevention or treatment of disorders associated with abnormal

CC function of the parathyroid gland or abnormal metabolism of calcium

CC and/or phosphate comprises parathyroid protein or an agent that

CC binds to the cis-acting element. It is useful for preventing

CC and/or treating over- or underproduction of PTH, bone diseases,

CC particularly osteoporosis, and for treating chronic renal failure.

CC A DNA construct comprising the cis-acting sequence with a coding

CC sequence is useful in gene therapy.

XX Sequence 18 BP; 10 A; 1 C; 2 G; 5 T; 0 other;

SQ Query Match 1.1%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 585 CTTATATGTAAGTATTA 602

Db 18 CTTCTTTTAAAGTATTA 1

RESULT 323

AAH63112/c

ID AAH63112 standard; DNA; 18 BP.

XX AAH63112;

XX 11-SEP-2001 (first entry)

XX Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 273.

DE Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;

KW antiviral agent; Gene expression; antisense construct; probe; primer;

KW transgenic viral resistant shrimp; ss.

XX White spot syndrome virus.

XX WO200138351-A2.

XX 31-MAY-2001.

XX 08-NOV-2000; 2000WO-US28888.

XX 24-NOV-1999; 99CN-0124717.

XX (PENY-) PE CORP NY.

XX (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.

XX (SINO-) SINOGENOMAX CO LTD.

XX Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;

XX WPI; 2001-355877/37.

XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus

PT (WSBV), useful for producing viral polypeptides that can be used to

PT screen for agents that are useful for treating WSBV infection -

XX Disclosure; Figure 3; 626pp; English.

XX The invention provides the primary nucleotide sequence of the WSBV genome

CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and

CC encoded proteins (AAH64910-AAH65051) and oligonucleotide sequences

CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid

CC molecules and proteins of the invention are useful for diagnosis and

CC monitoring viral infection, in screens for antiviral agents and for

CC monitoring viral gene expression or activity during a treatment regimen.

CC The nucleic acid molecules are also useful as antisense constructs to

XX	
OS	Human immunodeficiency virus type 1.
OS	Synthetic.

PN WO200255741-A2.
XX 18-JUL-2002.
XX 09-JAN-2002; 2002WO-EP00153.
XX 11-JAN-2001; 2001EP-0870005.
XX 20-APR-2001; 2001EP-0870085.
XX 24-APR-2001; 2001US-286102P.
XX (INNO-) INNOGENETICS NV.
XX De Smet K, Stuyver L;
XX WPI; 2002-590680/63.
XX
XX Detecting mutations associated with anti-HIV drug resistance comprises
XX detecting at least one of the mutations in the HIV reverse
XX transcriptase gene by using probes optimized to function together in a
XX reverse-hybridization assay
XX
XX Claim 2; Page 9; 117pp; English.
XX
XX The present invention describes a method for detecting mutations
XX associated with anti-HIV drug resistance in a patient by detecting at
XX least one of the mutations K103N/R, V106A/I/L, Y181C/I, Y188L,
XX G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
XX of HIV strains in a biological sample using a specific set of probes
XX optimised to function together in a reverse-hybridisation assay. The
XX method and the nucleic acid sequences used in the method are useful for
XX determining viral mutations and/or polymorphisms in the HIV RT gene
XX associated with resistance. The probes are useful for the genetic
XX detection, preferably in vitro detection of the mutations K103N/R,
XX V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
XX T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where
XX the mutation is associated with anti-HIV drug resistance. The method
XX provides a rapid, reliable and precise assay or determination and
XX monitoring of antiviral drug resistance or mutations associated with
XX drug resistance of viruses containing RT genes. ABZ33759 to ABZ34642
XX represent HIV RT sequences and probes which are used in the
XX exemplification of the present invention.
XX
XX Sequence 18 BP; 11 A; 2 C; 2 G; 3 T; 0 other;
XX
XX Query Match 1.1%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 3.8e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1570 TACTGTTTCGATGCTAT 1587
XX 18 TACTGTTTCGATGCTAT 1
XX
XX RESULT 327
XX ABL30677
XX ID ABL30677 standard; DNA; 18 BP.
XX
XX AC ABL30677;
XX
XX 21-MAR-2002 (first entry)
XX
XX Human HLA genotyping oligonucleotide SEQ ID NO 166.
XX
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
XX immunogenetic; transplantation; genetic disease; ss.
XX
XX Homo sapiens.
XX
XX WO200192572-A1.
XX
XX 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-JP04662.

XX 01-JUN-2000; 2000JP-0164798.
XX
XX (NISN) NISSHINO IND INC.
XX (SYST-) SYSTEM RES INC.
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes
XX of individuals e.g. by determining immunogenetic differences when
XX transplanting between them
XX
XX Claim 10; Page 124; 345pp; Japanese.
XX
XX The invention relates to a typing kit for judging human leukocyte antigen
XX (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
XX oligonucleotides (ABL30512-ABL31809) originating in the sequences of
XX genes e.g. belonging to HLA class I antigens on human genome and
XX containing gene polymorphisms as alloantigens have been immobilised as
XX primers for amplification of cleaved nucleic acids relating to gene
XX polymorphisms. The method is useful for judging HLA genotypes of
XX individuals by determining immunogenetic differences before transplanting
XX between them, providing genetic information to decide compatibility of
XX organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
XX pancreas, Langerhans islet in pancreas and cornea, susceptibility
XX diagnosis of genetic diseases and identifying individuals.
XX
XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 other;
XX
XX Query Match 1.1%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 3.8e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 519 GGTATTAATTTGAATTTC 536
XX 1 GCTTAACTTTGAANGTCA 18
XX
XX RESULT 328
XX ABX79935
XX ID ABX79935 standard; cDNA; 18 BP.
XX
XX AC ABX79935;
XX
XX 17-APR-2003 (first entry)
XX
XX EST polymorphic DNA repeat polynucleotide #260.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
XX
XX US6472154-B1.
XX
XX 29-OCT-2002.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.

PT Identifying a candidate polymorphic repeat within a coding sequence,
PT for understanding or treating genetic disease, comprises detecting
PT tandem repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability -
PS Examples; Column 1093; 588pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs.
XX
SQ Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 819 CTGGAATCTGGATT 836
|||||
DB 1 CTGGAACATGGATT 18

RESULT 329
ABZ10470
ID ABZ10470 standard; DNA; 18 BP.
XX
XX AC ABZ10470;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #610.

XX Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200277272-A2.
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-EP03401.
XX
XX 26-MAR-2001; 2001US-278333P.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Acor-Jan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
PI Pelet C, Schwabe I, Ziebarth H;
XX
XX WPI; 2003-018942/01.

XX Detecting and differentiating between haematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent
PT that distinguishes between methylated and non-methylated CpG
PT dinucleotides -
XX

PS Claim 15; Page 45; 117pp; English.

XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used; for
CC differentiating healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related
CC DNA sequences. The nucleotide sequences from the present invention can
CC also be used for detecting a predisposition to, differentiation between
CC subclases, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables
CC a highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients.
XX

SQ Sequence 18 BP; 7 A; 0 C; 4 G; 7 T; 0 other;

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1457 GTTATTATGTACAATA 1474
|||||
DB 1 GGTATTATGGATAATA 18

RESULT 330
ABC00856/C
ID ABC00856 standard; DNA; 13 BP.

XX
XX AC ABC00856;
XX
DT 20-FEB-2002 (first entry)
XX

DE Oligonucleotide SEQ ID NO 847 for detecting SNP TSC0000279.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX

PS Claim 1; SEQ ID 847; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 ATTAAACAAACAA 1216
Db 13 ATTAAACAAACAA 1

RESULT 331

ABC00857
ID ABC00857 standard; DNA; 13 BP.

XX ABC00857;

AC ABC00857;

DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 848 for detecting SNP TSC0000279.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX Claim 1; SEQ ID 848; 23pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 ATTAAACAAACAA 1216
Db 1 ATTAAACAAACAA 13

RESULT 332

ABC02380
ID ABC02380 standard; DNA; 13 BP.

XX ABC02380;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 2371 for detecting SNP TSC0000941.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX Claim 1; SEQ ID 2371; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABH99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1133 TTATAGTAAATTT 1145
Db 1 TTATAGTAAATTT 13

RESULT 333

ABC02381/C

ID ABC02381 standard; DNA; 13 BP.

XX AC ABC02381;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 2372 for detecting SNP TSC0000941.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 2372; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1133 TTATAGTAAATTT 1145
DB 13 TTATAGTAAATTT 1
RESULT 334
ABC08774/C
ID ABC08774 standard; DNA; 13 BP.
XX AC ABC08774;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 8765 for detecting SNP TSC0002388.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

PN WO200177384-A2.
XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 8765; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 0 A; 0 C; 2 G; 11 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 618 AAAAAACACAAA 630
DB 13 AAAAAACACAAA 1
RESULT 335
ABC08775
ID ABC08775 standard; DNA; 13 BP.
XX AC ABC08775;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 8766 for detecting SNP TSC0002388.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 8766; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABT00010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 11 A; 2 C; 0 G; 0 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 AAAAAACACAA 630

Db 1 AAAAAACACAA 13

RESULT 336

ABC18132
 ID ABC18132 standard; DNA; 13 BP.

AC ABC18132;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 18139 for detecting SNP TSC0003861.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 18139; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABT00010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 TTTAGTATAAGTA 1280

Db 1 TTTAGTATAAGTA 13

RESULT 337

ABC18133/c
 ID ABC18133 standard; DNA; 13 BP.

AC ABC18133;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 18140 for detecting SNP TSC0003861.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 18140; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

XX ABT00010-ABT82073 represent the oligomers described in the invention.

XX NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1268 TTAGTATAGTA 1280
Db 13 TTAGTATAGTA 1
|||||
RESULT 338
ABC19108/c
ID ABC19108 standard; DNA; 13 BP.
AC ABC19108;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 19125 for detecting SNP TSC0004001.
DE SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 19125 for detecting SNP TSC0004001.
DE SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 19125; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CCTATTATTATT 1048
Db 13 CCTATTATTATT 1
|||||
RESULT 339
ABC19109
ID ABC19109 standard; DNA; 13 BP.
XX
XX AC ABC19109;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 19457 for detecting SNP TSC0004047.
DE SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 19125; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CCTATTATTATT 1048
Db 13 CCTATTATTATT 1
|||||
RESULT 340
ABC19440
ID ABC19440 standard; DNA; 13 BP.
XX
XX AC ABC19440;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 19457 for detecting SNP TSC0004047.
DE SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF

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XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX CC Claim 1; SEQ ID 19457; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1049 TATGTATTATT 1061
XX DB 1 TATGTATTATT 13
XX
XX RESULT 341
XX ID ABC19441/C
XX AC ABC19441;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 19458 for detecting SNP TSC0004047.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX CC Claim 1; SEQ ID 19457; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1049 TATGTATTATT 1061
XX DB 1 TATGTATTATT 13
XX
XX RESULT 341
XX ID ABC19441/C
XX AC ABC19441;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 19458 for detecting SNP TSC0004047.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

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PS Claim 1; SEQ ID 19458; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 other;
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1049 TATGTATTATT 1061
XX DB 13 TATGTATTATT 1
XX
XX RESULT 342
XX ID ABC20820
XX AC ABC20820 standard; DNA; 13 BP.
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 20837 for detecting SNP TSC0004233.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX CC Claim 1; SEQ ID 20837; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1142 ATTTATTTATTT 1154
DB 1 ATTTATTTATTT 13

RESULT 343
ABC20821/c
ID ABC20821 standard; DNA; 13 BP.
XX
AC ABC20821;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 20838 for detecting SNP TSC0004233.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 20838; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1142 ATTTATTTATTT 1154
DB 13 ATTTATTTATTT 1

RESULT 344
ABC27496/c
ID ABC27496 standard; DNA; 13 BP.
XX
AC ABC27496;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 27513 for detecting SNP TSC0007650.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 27513; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 AACTATTAAACA 1408
DB 13 AACTATTAAACA 1

RESULT 345
ABC27497
ID ABC27497 standard; DNA; 13 BP.
XX
AC ABC27497;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 27514 for detecting SNP TSC0007650.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
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XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PS 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 27514; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABT00010-ABT99989 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1396 AACTATTAAACA 1408
XX DB 1 AACTATTAAACA 13
XX CC RESULT 346
XX CC ABC27750
XX ID ABC27750 standard; DNA; 13 BP.
XX AC ABC27750;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 27767 for detecting SNP TSC0007790.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 27514; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABT00010-ABT99989 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1396 AACTATTAAACA 1408
XX DB 1 AACTATTAAACA 13
XX CC RESULT 346
XX CC ABC27750
XX ID ABC27750 standard; DNA; 13 BP.
XX AC ABC27750;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 27767 for detecting SNP TSC0007790.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 27768; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

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PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 27767; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABT00010-ABT99989 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1295 TGAATTTTAATT 1307
XX DB 1 TGAATTTTAATT 13
XX CC RESULT 347
XX CC ABC27751/c
XX ID ABC27751 standard; DNA; 13 BP.
XX AC ABC27751;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 27768 for detecting SNP TSC0007790.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 27768; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

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CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABH82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1295 TGAATTTTAAAT 1307
 DB 13 TGAATTTTAAAT 1

RESULT 348
 ABC28094/C
 ID ABC28094 standard; DNA; 13 BP.

XX AC ABC28094;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 28111 for detecting SNP TSC0007954.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 28111; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABH00010-ABH82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 614 CTACAAAAACAA 626
 DB 13 CTACAAAAACAA 1

RESULT 349

ABC28095

XX AC ABC28095;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 28112 for detecting SNP TSC0007954.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status

XX Claim 1; SEQ ID 28112; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABH00010-ABH82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 614 CTACAAAAACAA 626
 DB 1 CTACAAAAACAA 13

RESULT 350

ABC29508

XX ID ABC29508 standard; DNA; 13 BP.

XX AC ABC29508;

PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 30127; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 9 A; 0 C; 1 G; 3 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 ATAAAGTAAATA 1606
DB 1 ATAAAGTAAATA 13

RESULT 353
ABC30111/c
ID ABC30111 standard; DNA; 13 BP.
XX ABC30111;
AC ABC30111;
XX
XX 20-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 30128 for detecting SNP TSC0009112.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 20-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 30128 for detecting SNP TSC0009112.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 30128; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 9 A; 0 C; 1 G; 3 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 ATAAAGTAAATA 1606
DB 1 ATAAAGTAAATA 13

RESULT 353
ABC30111/c
ID ABC30111 standard; DNA; 13 BP.
XX ABC30111;
AC ABC30111;
XX
XX 20-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 30128 for detecting SNP TSC0009112.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 30128; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 1 C; 0 G; 9 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 ATAAAGTAAATA 1606
DB 13 ATAAAGTAAATA 1

RESULT 354
ABC37546
ID ABC37546 standard; DNA; 13 BP.
XX ABC37546;
AC ABC37546;
XX
XX 20-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 37563 for detecting SNP TSC0011693.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 37563; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 6 A; 0 C; 2 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1123 TATAAGATGTTA 1135
|||||

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Db      1 TATAAAGATGTTA 13
RESULT 355
ABC37547/c
ID ABC37547 standard; DNA; 13 BP.
XX AC
XX AC ABC37547;
XX DT
XX DT 20-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide SEQ ID NO 37564 for detecting SNP TSC0011693.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PT
XX PS Claim 1; SEQ ID 37564; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX CC
XX SQ Sequence 13 BP; 5 A; 2 C; 0 G; 6 T; 0 other;
XX CC
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1123 TATAAAGATGTTA 1135
      |||||
Db      13 TATAAAGATGTTA 1
RESULT 356
ABC37938
ID ABC37938 standard; DNA; 13 BP.
XX AC
XX AC ABC37938;
XX DT
XX DT 20-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide SEQ ID NO 37955 for detecting SNP TSC0011786.

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KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PT
XX PS Claim 1; SEQ ID 37955; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX CC
XX SQ Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 other;
XX CC
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      752 AATGTGATATTG 764
      |||||
Db      1 AATGTGATATTG 13
RESULT 357
ABC37939/c
ID ABC37939 standard; DNA; 13 BP.
XX AC
XX AC ABC37939;
XX DT
XX DT 20-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide SEQ ID NO 37956 for detecting SNP TSC0011786.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR
XX PR 07-APR-2000; 2000DE-1019173.

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XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 37956; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 752 AATGTCATATTG 764
 DB 13 AATGTCATATTG 1
 RESULT 358
 ABC40556
 ID ABC40556 standard; DNA; 13 BP.
 XX ABC40556;
 AC 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 40573 for detecting SNP TSC0012288.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB00713.
 PF 07-APR-2000; 2000DE-1019173.
 PR (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 40573; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 TATATATATTATT 1493
 DB 1 TATATATATTATT 13
 RESULT 359
 ABC40557/c
 ID ABC40557 standard; DNA; 13 BP.
 XX ABC40557;
 AC 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 40574 for detecting SNP TSC0012288.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB00713.
 PF 07-APR-2000; 2000DE-1019173.
 PR (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 40574; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

```
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 TATAATATATTT 1493
Db 13 TATAATATATTT 1
|||||
RESULT 360
ABC55322
ID ABC55322 standard; DNA; 13 BP.
XX AC ABC55322;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55339 for detecting SNP TSC0015119.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX PS Claim 1; SEQ ID 55339; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX PS Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 600 TTATTATTGAA 612
Db 1 TTATTATTGAA 13
|||||
RESULT 361
ABC55323/c
ID ABC55323 standard; DNA; 13 BP.
XX AC ABC55323;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 61535 for detecting SNP TSC0016371.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

```
ID ABC55323 standard; DNA; 13 BP.
XX AC ABC55323;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55340 for detecting SNP TSC0015119.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX PS Claim 1; SEQ ID 55340; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX PS Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;
XX CC Query Match 1.0%; Score 13; DB 1; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 600 TTATTATTGAA 612
Db 13 TTATTATTGAA 1
|||||
RESULT 362
ABC61518
ID ABC61518 standard; DNA; 13 BP.
XX AC ABC61518;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 61535 for detecting SNP TSC0016371.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 61535; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABIC00010-ABIC02073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;
 XX Query Match 1.0%; Score 13; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1144 TTATTTTATTTTA 1156
 DB 1 TTATTTTATTTTA 13
 RESULT 363
 ABC61519/c
 ID ABC61519 standard; DNA; 13 BP.
 AC ABC61519;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 61536 for detecting SNP TSC0016371.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 61535; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABIC00010-ABIC02073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;
 XX Query Match 1.0%; Score 13; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1144 TTATTTTATTTTA 1156
 DB 1 TTATTTTATTTTA 13

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 61536; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABIC00010-ABIC02073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 other;
 XX Query Match 1.0%; Score 13; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1144 TTATTTTATTTTA 1156
 DB 13 TTATTTTATTTTA 1
 RESULT 364
 ABC61822/c
 ID ABC61822 standard; DNA; 13 BP.
 AC ABC61822;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 61839 for detecting SNP TSC0016434.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 61839; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 CAAAAAACACAA 629
 DB 13 CAAAAAACACAA 1

RESULT 365
 ABC61823
 ID ABC61823 standard; DNA; 13 BP.
 AC ABC61823;

XX 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 61840 for detecting SNP TSC0016434.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX

OS Homo sapiens.

XX WO200177384-A2.

FN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DB-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX Claim 1; SEQ ID 61840; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 10 A; 3 C; 0 G; 0 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 CAAAAAACACAA 629
 DB 1 CAAAAAACACAA 13

RESULT 366

ABC67270

ID ABC67270 standard; DNA; 13 BP.

XX ABC67270;

AC 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 67287 for detecting SNP TSC0017611.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX

OS Homo sapiens.

XX WO200177384-A2.

FN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DB-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX Claim 1; SEQ ID 67287; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 ATTAAATATATA 1625
 DB 1 ATTAAATATATA 13

RESULT 367

ABC67271/c

ID ABC67271 standard; DNA; 13 BP.

XX ABC67271;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 67288 for detecting SNP TSC0017611.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PT
XX Claim 1; SEQ ID 67288; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB102073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1613 ATTAAATATAA 1625
Db 13 ATTAAATATAA 1
RESULT 369
ABC72812/C
ID ABC72812 standard; DNA; 13 BP.
XX
XX ABC72812;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 72829 for detecting SNP TSC0018809.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX

PF 06-APR-2001; 2001WO-IB00713.
XX
FR 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PT
XX Claim 1; SEQ ID 72829; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB102073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1208 AACCAACAAACAA 1220
Db 13 AACCAACAAACAA 1
RESULT 369
ABC72813
ID ABC72813 standard; DNA; 13 BP.
XX
XX ABC72813;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 72830 for detecting SNP TSC0018809.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PT

XX PS Claim 1; SEQ ID 72830; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 10 A; 3 C; 0 G; 0 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 1208 AACAAACAACAA 1220
Db 1 AACAAACAACAA 13
|||||
1 AACAAACAACAA 13

RESULT 370
ABC78656
ID ABC78656 standard; DNA; 13 BP.
XX AC ABC78656;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 78673 for detecting SNP TSC0020028.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 78673; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 1134 TATAGTAATTTA 1146
Db 1 TATAGTAATTTA 13
|||||
1 TATAGTAATTTA 13

RESULT 371
ABC78657/C
ID ABC78657 standard; DNA; 13 BP.
XX AC ABC78657;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 78674 for detecting SNP TSC0020028.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status -
XX PS Claim 1; SEQ ID 78674; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1134 TATAGTAATTTA 1146
Db 13 TATAGTAATTTA 1
|||||
13 TATAGTAATTTA 1

XX PI Olek A, Piepenbrock C, Berlin K;
 DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 83569; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1046 ATTATGATTTA 1058
 DB 1 ATTATGATTTA 13
 RESULT 375
 ABC83553/c
 ID ABC83553 standard; DNA; 13 BP.
 AC ABC83553;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 83570 for detecting SNP TSC0021049.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 83570; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1046 ATTATGATTTA 1058
 DB 13 ATTATGATTTA 1
 RESULT 376
 ABC83568
 ID ABC83568 standard; DNA; 13 BP.
 AC ABC83568;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 83585 for detecting SNP TSC0021059.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 83585; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 TTATGATTATT 1060
|||||
DB 1 TTATGATTATT 13

RESULT 377
ABC83569/c
ID ABC83569 standard; DNA; 13 BP.
XX
AC ABC83569;
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 83586 for detecting SNP TSC0021059.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 83586; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
PS Sequence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 other;
XX
CC Query Match 1.0%; Score 13; DB 1; Length 13;
CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 TTATGATTATT 1060
|||||
DB 13 TTATGATTATT 1

RESULT 378
ABF01934
ID ABF01934 standard; DNA; 13 BP.
XX

AC ABF01934;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 101931 for detecting SNP TSC0025381.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 101931; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
PS Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 other;
XX
CC Query Match 1.0%; Score 13; DB 1; Length 13;
CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 GATGTTTATTGCT 1552
|||||
DB 1 GATGTTTATTGCT 13

RESULT 379
ABF01935/c
ID ABF01935 standard; DNA; 13 BP.
XX
AC ABF01935;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 101932 for detecting SNP TSC0025381.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

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XX PD 18-OCT-2001.
XX PF
XX PR 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX PS Claim 1; SEQ ID 101932; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1540 GAGGTTTTATGT 1552
XX DB 13 GAGGTTTTATGT 1
XX
XX RESULT 380
XX ABF12532/C
XX ID ABF12532 standard; DNA; 13 BP.
XX AC ABF12532;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 112529 for detecting SNP TSC0028137.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 21-FEB-2002 (first entry)
XX PR Oligonucleotide SEQ ID NO 112529 for detecting SNP TSC0028137.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX

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XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX PS Claim 1; SEQ ID 112529; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1139 TAAATTTATTTTA 1151
XX DB 13 TAAATTTATTTTA 1
XX
XX RESULT 381
XX ABF12533
XX ID ABF12533 standard; DNA; 13 BP.
XX AC ABF12533;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 112530 for detecting SNP TSC0028137.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX PS Claim 1; SEQ ID 112530; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC AB100010-AB182073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1139 TAAATTTATTTTA 1151
XX DB 13 TAAATTTATTTTA 1
XX
XX RESULT 381
XX ABF12533
XX ID ABF12533 standard; DNA; 13 BP.
XX AC ABF12533;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 112530 for detecting SNP TSC0028137.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX

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CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;

  Query Match      1.0%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 3.1e+02;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1139 TAAATTATTATTA 1151
Db 1 TAAATTATTATTA 13

RESULT 382
ABF15742/C
ID ABF15742 standard; DNA; 13 BP.
XX
AC ABF15742;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 115739 for detecting SNP TSC0029016.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 115739; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 other;

  Query Match      1.0%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 3.1e+02;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAACACAAATAA 633
```

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Db 13 AAACACAAATAA 1

RESULT 383
ABF15743
ID ABF15743 standard; DNA; 13 BP.
XX
AC ABF15743;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 115740 for detecting SNP TSC0029016.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 115740; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 10 A; 2 C; 0 G; 1 T; 0 other;

  Query Match      1.0%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 3.1e+02;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAACACAAATAA 633
Db 1 AAACACAAATAA 13

RESULT 384
ABF16636/C
ID ABF16636 standard; DNA; 13 BP.
XX
AC ABF16636;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 116633 for detecting SNP TSC0029186.
```


XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 116633; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI982073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TTATAATATTATT 1492
 DB 13 TTATAATATTATT 1
 RESULT 385
 ABF16637
 ID ABF16637 standard; DNA; 13 BP.
 XX AC ABF16637;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 116634 for detecting SNP TSC0029186.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 120439; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 116634; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI982073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TTATAATATTATT 1492
 DB 1 TTATAATATTATT 13
 RESULT 386
 ABF20442
 ID ABF20442 standard; DNA; 13 BP.
 XX AC ABF20442;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 120439 for detecting SNP TSC0030053.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 120439; 29pp + Sequence Listing; German.

```
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1050 ATGTATTATTATTA 1062
DB 1 ATGTATTATTATTA 13
|||||
RESULT 387
ABF20443/C
ID ABF20443 standard; DNA; 13 BP.
XX AC ABF20443;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 120440 for detecting SNP TSC0030053.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DS-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX Claim 1; SEQ ID 120440; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1050 ATGTATTATTATTA 1062
DB 1 ATGTATTATTATTA 13
|||||
RESULT 387
ABF20443/C
ID ABF20443 standard; DNA; 13 BP.
XX AC ABF20443;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 120440 for detecting SNP TSC0030053.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DS-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX Claim 1; SEQ ID 120440; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
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```
XX SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1050 ATGTATTATTATTA 1062
DB 13 ATGTATTATTATTA 1
|||||
RESULT 388
ABF20500
ID ABF20500 standard; DNA; 13 BP.
XX AC ABF20500;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 120497 for detecting SNP TSC0030072.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DS-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX Claim 1; SEQ ID 120497; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1140 AAATTATTATTAT 1152
DB 1 AAATTATTATTAT 13
|||||
RESULT 389
```

ABF20501/c
ID ABF20501 standard; DNA; 13 BP.
XX
AC ABF20501;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 120498 for detecting SNP TSC0030072.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
EN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 120498; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1140 AAATTTATTTAT 1152
DB 13 AAATTTATTTAT 1
XX
RESULT 396
ABF33284
ID ABF33284 standard; DNA; 13 BP.
XX
AC ABF33284;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 133281 for detecting SNP TSC0033254.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 133281; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1196 GTTTTATTTAT 1208
DB 1 GTTTTATTTAT 13
XX
RESULT 391
ABF33285/c
ID ABF33285 standard; DNA; 13 BP.
XX
AC ABF33285;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 133282 for detecting SNP TSC0033254.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

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XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1; SEQ ID 13282; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 other;
SQ
    Query Match      1.0%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 3.1e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1196 GTTTTAGATTAA 1208
DB      13 GTTTTAGATTAA 1
      |||||
      |||||

RESULT 392
ABF50618
ID      ABF50618 standard; DNA; 13 BP.
XX
XX AC      ABF50618;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 150615 for detecting SNP TSC0038010.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1; SEQ ID 150615; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

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CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 other;
SQ
    Query Match      1.0%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 3.1e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1537 TAAGATGTTTAA 1549
DB      1 TAAGATGTTTAA 13
      |||||
      |||||

RESULT 393
ABF50619/C
ID      ABF50619 standard; DNA; 13 BP.
XX
XX AC      ABF50619;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 150616 for detecting SNP TSC0038010.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1; SEQ ID 150616; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 other;
SQ
    Query Match      1.0%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 3.1e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


XX PF 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 160863; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1151 ATTTAGATATTA 1163
 DB 1 ATTTAGATATTA 13
 RESULT 397
 ABF60867/c
 ID ABF60867 standard; DNA; 13 BP.
 XX AC ABF60867;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 160864 for detecting SNP TSC0040506.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 160863; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1151 ATTTAGATATTA 1163
 DB 1 ATTTAGATATTA 13

PT methylation status
 XX Claim 1; SEQ ID 160864; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1151 ATTTAGATATTA 1163
 DB 13 ATTTAGATATTA 1
 RESULT 398
 ABF65362/c
 ID ABF65362 standard; DNA; 13 BP.
 XX AC ABF65362;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 165359 for detecting SNP TSC0041473.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX Claim 1; SEQ ID 165359; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1616 TAAATATTAATTT 1628

Db 13 TAAATATTAATTT 1

RESULT 399

ABF65363
 ID ABF65363 standard; DNA; 13 BP.

XX AC ABF65363;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 165360 for detecting SNP TSC0041473.

XX KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX PS Claim 1; SEQ ID 165360; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

XX CC ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.

XX CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1616 TAAATATTAATTT 1628

Db 1 TAAATATTAATTT 13

RESULT 400

ABF68619/c

ID ABF68619 standard; DNA; 13 BP.

XX AC ABF68619;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 168615 for detecting SNP TSC0008285.

XX KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX PS Claim 1; SEQ ID 168615; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

XX CC ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.

XX CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 8 A; 0 C; 1 G; 4 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 ATTTTAACTTTA 1538

Db 13 ATTTTAACTTTA 1

RESULT 401

ABF68619

ID ABF68619 standard; DNA; 13 BP.

XX AC ABF68619;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 168616 for detecting SNP TSC0008285.

XX KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 168616; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 other;
 XX Query Match 1.0%; Score 13; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1526 ATTTTAACTTTA 1538
 DB 1 ATTTTAACTTTA 13
 RESULT 402
 ABF71788
 ID ABF71788 standard; DNA; 13 BP.
 XX AC ABF71788;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 171785 for detecting SNP TSC0042822.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 171786; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 171785; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
 XX Query Match 1.0%; Score 13; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 633 ATTTTGAATATA 645
 DB 1 ATTTTGAATATA 13
 RESULT 403
 ABF71789/c
 ID ABF71789 standard; DNA; 13 BP.
 XX AC ABF71789;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 171786 for detecting SNP TSC0042822.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 171786; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 633 ATTTTGGATATA 645
 Db 13 ATTTTGGATATA 1

RESULT 404

ABF83258
 ID ABF83258 standard; DNA; 13 BP.

XX
 AC ABF83258;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 183255 for detecting SNP TSC0045246.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX Claim 1; SEQ ID 183255; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC AB100010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 AATAATTTTGAA 641
 Db 1 AATAATTTTGAA 13

RESULT 405

ABF83259/C
 ID ABF83259 standard; DNA; 13 BP.

XX
 AC ABF83259;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 183256 for detecting SNP TSC0045246.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX Claim 1; SEQ ID 183256; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC AB100010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 AATAATTTTGAA 641
 Db 13 AATAATTTTGAA 1

RESULT 406

ABF83902/C
 ID ABF83902 standard; DNA; 13 BP.

XX ABF83902;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 183899 for detecting SNP TSC0004785.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 183899; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 611 AATCTACAAAAA 623
Db 13 AATCTACAAAAA 1
RESULT 407
ABF83903
ID ABF83903 standard; DNA; 13 BP.
AC
XX ABF83903;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 183900 for detecting SNP TSC0004785.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 183899; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 611 AATCTACAAAAA 623
Db 13 AATCTACAAAAA 1
RESULT 407
ABF83903
ID ABF83903 standard; DNA; 13 BP.
AC
XX ABF83903;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 183900 for detecting SNP TSC0004785.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX

PN WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 183900; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 611 AATCTACAAAAA 623
Db 1 AATCTACAAAAA 13
RESULT 408
ABF8502
ID ABF8502 standard; DNA; 13 BP.
AC
XX ABF8502;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 188499 for detecting SNP TSC0046423.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB00713.
PF
XX 07-APR-2000; 2000DE-1019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 188499; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1618 AAATATAATTGT 1630
XX 1 AAATATAATTGT 13
XX
XX RESULT 409
XX ABF88503/C
XX ID ABF88503 standard; DNA; 13 BP.
XX AC ABF88503;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DZ Oligonucleotide SEQ ID NO 188500 for detecting SNP TSC0046423.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX KW
XX OS Homo sapiens.
XX OS
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX XX
XX PR 07-APR-2000; 2000DE-1019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX XX
XX PS Claim 1; SEQ ID 188500; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1618 AAATATAATTGT 1630
XX 13 AAATATAATTGT 1
XX
XX RESULT 410
XX ABF94864
XX ID ABF94864 standard; DNA; 13 BP.
XX AC ABF94864;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DZ Oligonucleotide SEQ ID NO 194861 for detecting SNP TSC0005457.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX KW
XX OS Homo sapiens.
XX OS
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX XX
XX PR 07-APR-2000; 2000DE-1019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX XX
XX PS Claim 1; SEQ ID 194861; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

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QY      1197  TTTTAGATTAAA 1209
DB      1  TTTTAGATTAAA 13
|||||
|||||

RESULT 411
ABF94865/c
ABF94865 standard; DNA; 13 BP.
XX
AC  ABF94865;
XX
DT  22-FEB-2002 (first entry)
XX
XX  Oligonucleotide SEQ ID NO 194862 for detecting SNP TSC0005457.
DE
XX  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX  Homo sapiens.
XX
XX  WO200177384-A2.
XX
XX  18-OCT-2001.
XX
XX  06-APR-2001; 2001WO-IB00713.
XX
XX  07-APR-2000; 2000DE-1019173.
XX
XX  (EPIG-) EPIGENOMICS AG.
XX
XX  Olek A, Piepenbrock C, Berlin K;
PI
XX  WPI; 2001-657177/75.
XX
XX  Set of oligonucleotides, useful for diagnosis and cell typing, is
XX  designed to detect single nucleotide polymorphisms and cytosine
XX  methylation status
XX
XX  Claim 1; SEQ ID 194862; 29pp + Sequence Listing; German.
XX
XX  This invention describes novel oligonucleotide primers or peptide nucleic
XX  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX  and cytosine methylation status in chemically pretreated genomic DNA. The
XX  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX  range of diseases including immune system, gastrointestinal, respiratory,
XX  central nervous system, cardiovascular and metabolic disorders. The
XX  oligomers are also used for detecting cell type differentiation.
XX  ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX  ABJ00010-ABI82073 represent the oligomers described in the invention.
XX  NOTE: The sequence data for this patent did not form part of the printed
XX  specification, but was obtained in electronic format from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences.
XX
XX  Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
XX
XX  Query Match 1.0%; Score 13; DB 1; Length 13;
XX  Best Local Similarity 100.0%; Pred. NO. 3.1e+02;
XX  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX

QY      1197  TTTTAGATTAAA 1209
DB      13  TTTTAGATTAAA 1
|||||
|||||

RESULT 412
ABH13810
ID  ABH13810 standard; DNA; 13 BP.
XX
AC  ABH13810;
XX
XX  22-FEB-2002 (first entry)
XX
XX

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XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 213788; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX ABT00010-ABT82073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1536 TTAAGATGTTTTT 1548
 DB 13 TTAAGATGTTTTT 1
 |||||
 RESULT 414
 ABH231148
 ID ABH231148 standard; DNA; 13 BP.
 AC ABH231148;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 223125 for detecting SNP TSC0054328.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 213788; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX ABT00010-ABT82073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1536 TTAAGATGTTTTT 1548
 DB 13 TTAAGATGTTTTT 1
 |||||
 RESULT 414
 ABH231148
 ID ABH231148 standard; DNA; 13 BP.
 AC ABH231148;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 223125 for detecting SNP TSC0054328.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -

PS Claim 1; SEQ ID 223125; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX ABT00010-ABT82073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1136 TAGTAAATTTATT 1148
 DB 1 TAGTAAATTTATT 13
 |||||
 RESULT 415
 ABH231149/c
 ID ABH231149 standard; DNA; 13 BP.
 AC ABH231149;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 223126 for detecting SNP TSC0054328.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 223126; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX ABT00010-ABT82073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at

```

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1136 TAGTAATTTATT 1148
   |||||
Db 13 TAGTAATTTATT 1

RESULT 416
ABH27672
ID ABH27672 standard; DNA; 13 BP.
XX
AC ABH27672;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 227649 for detecting SNP TSC0055515.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
PS Claim 1; SEQ ID 227649; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 TCGAATATATAAA 1599
   |||||
Db 1 TCGAATATATAAA 13

RESULT 417
ABH27673/c
ID ABH27673 standard; DNA; 13 BP.
XX
AC ABH27673;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 227650 for detecting SNP TSC0055515.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
PS Claim 1; SEQ ID 227650; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 TCGAATATATAAA 1599
   |||||
Db 13 TCGAATATATAAA 13

RESULT 418
ABH29396
ID ABH29396 standard; DNA; 13 BP.
XX
AC ABH29396;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 229373 for detecting SNP TSC00555957.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX PS Claim 1; SEQ ID 229373; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1045 TATTATGATTT 1057
Db 1 TATTATGATTT 13

RESULT 419
ABH29397/C
ID ABH29397 standard; DNA; 13 BP.
AC ABH29397;
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 229374 for detecting SNP TSC055957.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.

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PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX PS Claim 1; SEQ ID 229374; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1045 TATTATGATTT 1057
Db 13 TATTATGATTT 1

RESULT 420
ABH37864
ID ABH37864 standard; DNA; 13 BP.
XX
XX ABH37864;
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 237841 for detecting SNP TSC0058010.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX PS Claim 1; SEQ ID 237841; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

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CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 GGGTTTTCAGTT 1206
DB 1 GGGTTTTCAGTT 13
RESULT 421
ABH37865/C
ID ABH37865 standard; DNA; 13 BP.
XX
AC ABH37865;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 237842 for detecting SNP TSC0058010.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 237842; 29pp + Sequence Listing; German.
XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1194 GGGTTTTCAGTT 1206
DB 13 GGGTTTTCAGTT 1

RESULT 422
ABH48890
ID ABH48890 standard; DNA; 13 BP.
XX
AC ABH48890;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 248867 for detecting SNP TSC0060809.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 248867; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1146 ATTTATTTTACA 1158
DB 1 ATTTATTTTACA 13

RESULT 423
ABH48891/C
ID ABH48891 standard; DNA; 13 BP.
XX
AC ABH48891;


```

PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
PS Claim 1; SEQ ID 243464; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1205 TTAACACAAACAA 1217
DB 1 TTAACACAAACAA 13
RESULT 426
ABH53272/C
ID ABH53272 standard; DNA; 13 BP.
XX
AC ABH53272;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 253249 for detecting SNP TSC0061766.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
PS Claim 1; SEQ ID 253249; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1205 TTAACACAAACAA 1217
DB 1 TTAACACAAACAA 13
RESULT 427
ABH53273
ID ABH53273 standard; DNA; 13 BP.
XX
AC ABH53273;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 253250 for detecting SNP TSC0061766.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
PS Claim 1; SEQ ID 253250; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1558 CCAAAATTTTTTTT 1570
DB 13 CCAAAATTTTTTTT 1

```

```

Db      1 CCACATTTTITTT 13
RESULT 428
ABH53668/c
ID ABH53668 standard; DNA; 13 BP.
XX
XX AC ABH53668;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 253645 for detecting SNP TSC0061845.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 253645; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      622 AACACCAATAAT 634
Db      13 AACACCAATAAT 1
|||||
|

RESULT 429
ABH53669
ID ABH53669 standard; DNA; 13 BP.
XX
XX AC ABH53669;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 253646 for detecting SNP TSC0061845.
XX

```

```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 253646; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      622 AACACCAATAAT 634
Db      1 AACACCAATAAT 13
|||||
|

RESULT 430
ABH55558
ID ABH55558 standard; DNA; 13 BP.
XX
XX AC ABH55558;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 255535 for detecting SNP TSC0062287.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX

```

XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 255535; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1427 ATATTAGTAATTT 1439
 DB 1 ATATTAGTAATTT 13
 RESULT 431
 ABH55559/C
 ID ABH55559 standard; DNA; 13 BP.
 AC ABH55559;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 255536 for detecting SNP TSC0062287.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 255536; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1427 ATATTAGTAATTT 1439
 DB 13 ATATTAGTAATTT 1
 RESULT 432
 ABH57674
 ID ABH57674 standard; DNA; 13 BP.
 AC ABH57674;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 257651 for detecting SNP TSC0062680.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 257651; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1427 ATATTAGTAATTT 1439
 DB 13 ATATTAGTAATTT 1
 RESULT 432
 ABH57674
 ID ABH57674 standard; DNA; 13 BP.
 AC ABH57674;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 257651 for detecting SNP TSC0062680.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 257651; 29pp + Sequence Listing; German.

```

SQ Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1163 AAATGATGTTTAA 1175
Db 1 AAATGATGTTTAA 13

RESULT 433
ABH57675/c
ID ABH57675 standard; DNA; 13 BP.
AC ABH57675;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 257652 for detecting SNP TSC0062680.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX Oligonucleotide SEQ ID NO 257652 for detecting SNP TSC0062680.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 257652; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1163 AAATGATGTTTAA 1175
Db 13 AAATGATGTTTAA 1

RESULT 434
ABH58412

```

```

ID ABH58412 standard; DNA; 13 BP.
XX
AC ABH58412;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 258389 for detecting SNP TSC0062829.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 258389; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1486 TATTATTAAATG 1498
Db 1 TATTATTAAATG 13

RESULT 435
ABH58413/c
ID ABH58413 standard; DNA; 13 BP.
XX
AC ABH58413;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 258390 for detecting SNP TSC0062829.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.

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XX PN WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX XX designed to detect single nucleotide polymorphisms and cytosine
XX XX methylation status -
XX XX Claim 1; SEQ ID 258390; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX XX range of diseases including immune system, gastrointestinal, respiratory,
XX XX central nervous system, cardiovascular and metabolic disorders. The
XX XX oligomers are also used for detecting cell type differentiation.
XX XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX XX AB100010-AB182073 represent the oligomers described in the invention.
XX XX NOTE: The sequence data for this patent did not form part of the printed
XX XX specification, but was obtained in electronic format from WIPO at
XX XX ftp.wipo.int/pub/published_pct_sequences.
XX XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1486 TATTATTAAATG 1498
XX DB 13 TATTATTAAATG 1
XX
XX RESULT 436
XX ABH62638
XX ID ABH62638 standard; DNA; 13 BP.
XX AC ABH62638;
XX XX 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 262615 for detecting SNP TSC0009751.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
XX XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX XX designed to detect single nucleotide polymorphisms and cytosine
XX XX methylation status -
XX XX Claim 1; SEQ ID 258390; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX XX range of diseases including immune system, gastrointestinal, respiratory,
XX XX central nervous system, cardiovascular and metabolic disorders. The
XX XX oligomers are also used for detecting cell type differentiation.
XX XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX XX AB100010-AB182073 represent the oligomers described in the invention.
XX XX NOTE: The sequence data for this patent did not form part of the printed
XX XX specification, but was obtained in electronic format from WIPO at
XX XX ftp.wipo.int/pub/published_pct_sequences.
XX XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1486 TATTATTAAATG 1498
XX DB 13 TATTATTAAATG 1
XX
XX RESULT 436
XX ABH62638
XX ID ABH62638 standard; DNA; 13 BP.
XX AC ABH62638;
XX XX 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 262615 for detecting SNP TSC0009751.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
XX XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX XX designed to detect single nucleotide polymorphisms and cytosine
XX XX methylation status -
XX XX Claim 1; SEQ ID 262616; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX XX range of diseases including immune system, gastrointestinal, respiratory,
XX XX central nervous system, cardiovascular and metabolic disorders. The
XX XX oligomers are also used for detecting cell type differentiation.
XX XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX XX AB100010-AB182073 represent the oligomers described in the invention.
XX XX NOTE: The sequence data for this patent did not form part of the printed
XX XX specification, but was obtained in electronic format from WIPO at
XX XX ftp.wipo.int/pub/published_pct_sequences.
XX XX Query Match 1.0%; Score 13; DB 1; Length 13;
XX XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1586 ATGGAAATATATA 1598
XX DB 1 ATGGAAATATATA 13
XX
XX RESULT 437
XX ABH62639/C
XX ID ABH62639 standard; DNA; 13 BP.
XX AC ABH62639;
XX XX 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 262616 for detecting SNP TSC0009751.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
XX XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX XX designed to detect single nucleotide polymorphisms and cytosine
XX XX methylation status -
XX XX Claim 1; SEQ ID 262616; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX XX range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABT00010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1586 ATGGAAATATATAA 1598
 Db 13 ATGGAAATATATAA 1

RESULT 438
 ABH66082/c
 ID ABH66082 standard; DNA; 13 BP.
 XX
 AC ABH66082;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 266059 for detecting SNP TSC0064472.
 XX
 SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 WO200177384-A2.
 XX
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 266059; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABT00010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 13 BP; 8 A; 0 C; 1 G; 4 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 TATATTTTAACT 1535
 Db 13 TATATTTTAACT 1

RESULT 439
 ABH66083
 ID ABH66083 standard; DNA; 13 BP.
 XX
 AC ABH66083;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 266060 for detecting SNP TSC0064472.
 XX
 SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 WO200177384-A2.
 XX
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 266060; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABT00010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 TATATTTTAACT 1535
 Db 1 TATATTTTAACT 13

RESULT 440
 AAT56348
 ID AAT56348 standard; RNA; 15 BP.
 XX
 AC AAT56348;
 XX
 DT 25-MAR-2003 (updated)


```

PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them -
PT for use in inhibiting disease related genes
XX
PS Claim 2; Page 252; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme), which cleaves TNF-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1038 TATTATTATTATTA 1050
Db 3 UAUUUUAUUUUA 15
RESULT 442
AAT55809
ID AAT55809 standard; RNA; 15 BP.
AC AAT55809;
XX
DT 25-MAR-2003 (updated)
DT 25-MAR-1997 (first entry)
XX
DE Human TNF-alpha hammerhead ribozyme target sequence (nt position 1267).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS; 88.
XX
OS Homo sapiens.
XX
PN W09523225-A2.
XX
PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB00156.

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XX 30-JAN-1995; 94US-0380734.
XX 23-FEB-1994; 94US-0201109.
XX 29-MAR-1994; 94US-0218934.
XX 04-APR-1994; 94US-0222795.
XX 07-APR-1994; 94US-0224483.
XX 15-APR-1994; 94US-0227958.
XX 15-APR-1994; 94US-0228041.
XX 18-MAY-1994; 94US-0245736.
XX 06-JUL-1994; 94US-0271280.
XX 15-AUG-1994; 94US-0291932.
XX 16-AUG-1994; 94US-0291433.
XX 17-AUG-1994; 94US-0294620.
XX 19-AUG-1994; 94US-0293520.
XX 02-SEP-1994; 94US-0300000.
XX 08-SEP-1994; 94US-0303039.
XX 23-SEP-1994; 94US-0311486.
XX 23-SEP-1994; 94US-0311749.
XX 28-SEP-1994; 94US-0314397.
XX 03-OCT-1994; 94US-0316771.
XX 07-OCT-1994; 94US-0319492.
XX 11-OCT-1994; 94US-0321993.
XX 04-NOV-1994; 94US-0334847.
XX 10-NOV-1994; 94US-0337608.
XX 28-NOV-1994; 94US-0345516.
XX 15-DEC-1994; 94US-0352577.
XX 23-DEC-1994; 94US-0363233.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them -
XX for use in inhibiting disease related genes
XX
XX Claim 2; Page 243; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme), which cleaves TNF-alpha
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
Qy 1038 TATTATTATTATTA 1050
Db 3 UAUUUUAUUUUA 15
RESULT 443
AAT55794
ID AAT55794 standard; RNA; 15 BP.
XX
AC AAT55794;

```

XX 25-MAR-2003 (updated)
 DT 25-MAR-1997 (first entry)
 XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1256).
 DE
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9523225-A2.
 XX
 XX 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 16-AUG-1994; 94US-0291932.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 23-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowrira B, Ditzon A, Draper KG, Dudycz LW;
 PI Grimm S, Karpaisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR
 XX Ribozymes having modified bases and methods for producing them
 PT for use in inhibiting disease related genes
 XX
 XX Claim 2; Page 242; 407pp; English.
 PS
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.

CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 15;
 Best Local Similarity 30.8%; Pred No. 3.5e+02;
 Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 QY 1038 TATTATTATTATTA 1050
 Db :|::|::|::|::|
 3 UAUUUUUUUUA 15
 RESULT 444
 AAT57265/C
 ID AAT57265 standard; RNA; 15 BP.
 XX
 AC AAT57265;
 XX
 DT 25-MAR-2003 (updated)
 DT 15-MAR-1997 (first entry)
 DE RSV N hammerhead ribozyme target sequence (nt. position 383).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Respiratory Syncytial Virus.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 16-AUG-1994; 94US-0291932.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 23-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.

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PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345536.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowira B, Diranzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpelsky A, Kleich K, Matulic-adamic J, Meswiggen JA;
PI Modak A, Pavco P, Belgienan L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott PE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them
PT for use in inhibiting disease related genes
XX
XX Claim 2; Page 274; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding
CC for a protein of respiratory syncytial virus (RSV) at the
CC nucleotide base position indicated in the DE line. Regions of
CC the mRNA that do not form secondary folding structures and that
CC contain potential hammerhead and hairpin ribozyme cleavage sites
CC were identified by computer analysis. Ribozymes directed against
CC these mRNA sequences were designed and synthesised with modifications
CC that improve their nuclease resistance. The ribozymes cleave the
CC target sequences and can be used for treatment and diagnosis of
CC RSV infection.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 15 BP; 7 A; 3 C; 1 G; 4 U; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 525 ATTGAATTTCAG 537
DB 13 ATTGAATTTCAG 1
RESULT 445
AAT93825/C
ID AAT93825 standard; DNA; 15 BP.
XX
XX AAT93825;
XX
XX 25-MAR-2003 (updated)
DT 24-FEB-1998 (first entry)
XX
XX Antitumoural phosphodiester oligonucleotide 15 with cytotoxic activity.
DE
XX Phosphodiester; selective binding; cell viability; growth;
KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW lymphoblastic tumour; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..15
FT /tag= a
FT /note= "phosphodiester oligonucleotide"
XX
XX W09720924-A1.
PN
XX 12-JUN-1997.
PD
XX 04-DEC-1996; 96WO-EP05388.
PP
XX 04-DEC-1995; 95IT-MT02539.
XX
XX

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PA (SAIC-) SAICOM SRL.
XX
XX Quadrifoglio P, Scaggiante B;
XX
XX WPI; 1997-319771/29.
XX
XX New phosphodiesteric oligonucleotide(s) - which exert a specific
PT and selective cytotoxic effect on tumour cells, for treating both
PT solid and liquid tumours
XX
XX Claim 10; Page 6; 38pp; English.
XX
XX Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC generic formula, in the 3'-5' or 5'-3' direction:
CC (GatA')a''-(Gbtb')b''-(Gctc')c''-(Gdtd')d''-(Gete')e''-(Gftf')f''-
CC (Ggtg')g''-N', where:
CC N and N' = T or G, equal or different from each other;
CC x = 0-8, equal or different from each other;
CC a, b, c, d, e, f, and g = 0-10, equal or different from each other;
CC a', b', c', d', e', f', and g' = 0-30, equal or different from each
CC other;
CC a'', b'', c'', d'', e'', f'', and g'' = 1-16, equal or different from
CC each other;
CC The oligonucleotides are believed to selectively bind and sequester
CC some proteins which are essential to the viability and growth of
CC tumoural cell line. They have specific and selective cytotoxic activity
CC against tumour cells, and can be used for treating tumours of the liquid
CC type, in particular of lymphoblastic origin, and of solid type, in
CC particular lymphomas.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 4 G; 11 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1207 AAACAACCAACA 1219
DB 13 AAACAACCAACA 1
RESULT 445
AAF70068
ID AAF70068 standard; DNA; 15 BP.
XX
XX AAF70068;
XX
XX 18-APR-2001 (first entry)
DT
XX Human TNFRSF11B gene ASO probe, SEQ ID NO: 124.
DE
XX Human; TNFRSF11B; osteoclastogenesis inhibitory factor;
KW single nucleotide polymorphism; SNP; osteoclast recruitment;
KW osteoclast function; osteoporosis; metastatic bone disease;
KW Paget's disease; rheumatoid arthritis; periodontal bone disease;
KW ASO; allele-specific oligonucleotide; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200104137-A1.
PN
XX 18-JAN-2001.
PD
XX 10-JUL-2000; 2000WO-US18503.
PF
XX 09-JUL-1999; 99US-0143020.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI WPI; 2001-147175/15.
DR

```

XX Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising
PT single nucleotide polymorphisms, useful for studying e.g. osteoporosis,
PT Paget's disease and rheumatoid arthritis -
XX
XX Claim 15; Page 23; 114pp; English.
XX
XX The present sequence is a probe used to detect polymorphisms in the human
CC osteoclastogenesis inhibitory factor (TNFRSF11B). Polynucleotides
CC comprising one or more of twenty four novel single nucleotide
CC polymorphisms in the TNFRSF11B gene have been identified. TNFRSF11B
CC regulate osteoclast recruitment and function. An understanding of
CC variations in the gene should thus be useful in developing new therapies
CC for metabolic disorders caused by abnormal osteoclast recruitment and
CC function such as osteoporosis, metastatic bone disease, Paget's disease,
CC rheumatoid arthritis and periodontal bone disease.
XX
XX Sequence 15 BP; 4 A; 0 C; 1 G; 10 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1147 TTTTATTATTAGAT 1159
Db 1 TTTTATTATTAGAT 13
RESULT 447
AAFT0070
ID AAF70070 standard; DNA; 15 BP.
AC
XX
XX AAF70070;
DT 18-APR-2001 (first entry)
DE Human TNFRSF11B gene ASO probe, SEQ ID NO: 126.
XX
XX Human; TNFRSF11B; osteoclastogenesis inhibitory factor;
KW single nucleotide polymorphism; SNP; osteoclast recruitment;
KW osteoclast function; osteoporosis; metastatic bone disease;
KW Paget's disease; rheumatoid arthritis; periodontal bone disease;
KW ASO; allele-specific oligonucleotide; probe; ss.
XX
XX Homo sapiens.
OS
XX WO200104137-A1.
PN
XX 18-JAN-2001.
PD
XX 10-JUL-2000; 2000WO-US18803.
PF
XX 09-JUL-1999; 99US-0143020.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Chew A, Denton RE, Duda A, Nandabalan K, Stephens JC;
PI WPI; 2001-147175/15.
XX
XX Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising
PT single nucleotide polymorphisms, useful for studying e.g. osteoporosis,
PT Paget's disease and rheumatoid arthritis -
XX
XX Claim 15; Page 23; 114pp; English.
XX
XX The present sequence is a probe used to detect polymorphisms in the human
CC osteoclastogenesis inhibitory factor (TNFRSF11B). Polynucleotides
CC comprising one or more of twenty four novel single nucleotide
CC polymorphisms in the TNFRSF11B gene have been identified. TNFRSF11B
CC regulate osteoclast recruitment and function. An understanding of
CC variations in the gene should thus be useful in developing new therapies
CC for metabolic disorders caused by abnormal osteoclast recruitment and

CC function such as osteoporosis, metastatic bone disease, Paget's disease,
CC rheumatoid arthritis and periodontal bone disease.
XX
XX Sequence 15 BP; 4 A; 0 C; 2 G; 9 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1147 TTTTATTATTAGAT 1159
Db 1 TTTTATTATTAGAT 13
RESULT 448
ABT04008/C
ID ABT04008 standard; DNA; 15 BP.
XX
XX AC ABT04008;
XX
XX 25-SEP-2002 (first entry)
DT
DE Human ovary specific coding sequence SEQ ID NO: 27.
XX
XX Human; ovary; ovarian cancer; ovarian disease; gene therapy; gene;
KW cytostatic; ds.
XX
XX Homo sapiens.
OS
XX WO200240720-A2.
PN
XX 23-MAY-2002.
PD
XX 20-NOV-2001; 2001WO-US45010.
PF
XX 20-NOV-2000; 2000US-249997P.
PR
XX (DIAD-) DIADEXUS INC.
PA
XX Saiceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu C;
PI WPI; 2002-547588/58.
XX
XX New ovary polypeptides useful for detecting, diagnosing, monitoring,
PT treating, staging and imaging cancers in humans having cancer and
PT non-cancerous ovary disease -
XX
XX Claim 1; Page 162; 296pp; English.
XX
XX The present invention provides human proteins and coding sequences
CC specifically found in ovary cells. These can be used in the diagnosis and
CC treatment of ovarian diseases, including cancer. The present sequence is
CC a coding sequence of the invention.
XX
XX Sequence 15 BP; 11 A; 0 C; 0 G; 4 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1038 TATTATTATTATTA 1050
Db 13 TATTATTATTATTA 1
RESULT 449
AAQ23015/C
ID AAQ23015 standard; DNA; 17 BP.
XX
XX AC AAQ23015;
XX
XX 25-MAR-2003 (updated)
DT 19-NOV-1992 (first entry)

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XX Pro-UK probe T6 (Td = 52).
XX Prourokinase; vascular endothelial cell; ss.
XX Synthetic.
XX JP04053489-A.
XX 21-FEB-1992.
XX 21-JUN-1990; 90JP-0163144.
XX 21-JUN-1990; 90JP-0163144.
XX (TAIS ) TAISHO PHARM CO LTD.
XX WPI; 1992-110627/14.
XX Efficient prodn. of pro-urokinase by genetic engineering - by
XX transforming host cell by expression vector of deoxyribonucleic
XX acid of human vascular endothelial cell, and culturing
XX Disclosure; Fig 8; 16pp; Japanese.
XX The probes represented in AAQ23010-15 were used in the prodn. of
XX human pro-UK cDNA (example 3 (page 7)).
XX Prepn. of pro-UK comprises transforming a host cell with an
XX expression vector contg. cDNA encoding pro-UK, derived from human
XX vascular endothelial cells. The resultant transformant is cultured.
XX The new type of pro-UK can be produced efficiently in large amts.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 17 BP; 8 A; 4 C; 5 G; 0 U; 0 Other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1437 TTTCCTGCTGGTT 1449
DB 13 TTTCCTGCTGGTT 1

RESULT 450
AAQ65895/c
ID AAQ65895 standard; DNA; 17 BP.
XX AC AAQ65895;
XX 25-MAR-2003 (updated)
XX 22-DEC-1994 (first entry)
XX Type II procollagen sequencing primer 86.
XX Type II procollagen; COL2A1; amplification; primer;
XX polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.
XX Synthetic.
XX W09411532-A1.
XX 26-MAY-1994.
XX 12-NOV-1993; 93WO-US10964.
XX 13-NOV-1992; 92US-0977284.
XX (UJVB-) UNIV JEFFERSON THOMAS.
XX Ahmad NN, Ala-Kokko L, Baldwin C, Hopkinson I, Prockop DJ;
XX Ritvaniemi P, Williams CJ;

WPI; 1994-183530/22.
XX Detecting genetic pre-disposition to osteoarthritis - and other
XX diseases involving mutation in cartilage protein genes, by
XX amplification and analysis of DNA and comparison with standards
XX Claim 18; Page 30; 112pp; English.
XX Claim 18 claims primers for use in detecting mutations in a
XX mammalian gene for a structural protein of cartilage comprising
XX a sequence identified in Table I (Page 18-31). Table I includes
XX 179 primer sequences (see AAQ65728-Q65906).
XX The following details are given for primer 86:
XX Alt. code: DH-78
XX Region/exon: 49
XX Direction: sense
XX Primer position: 20135
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 TTTCCTAGATGT 756
DB 15 TTTCCTAGATGT 3

RESULT 451
AAV97734
ID AAV97734 standard; RNA; 17 BP.
XX AC AAV97734;
XX 17-MAR-1999 (first entry)
XX Human EGF-R target sequence nucleotide position 4156.
XX Human; epidermal growth factor receptor; EGF-R; target sequence;
XX hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
XX cancer; Genetic drift; detection; mutation; ss.
XX OS Homo sapiens.
XX W09833893-A2.
XX 06-AUG-1998.
XX 14-JAN-1998; 98WO-US00730.
XX 04-DEC-1997; 97US-0985162.
XX 31-JAN-1997; 97US-0036476.
XX (RIBO-) RIBOZYME PHARM INC.
XX (UYAS-) UNIV ASTON.
XX Akhtar S, Fell P, McSwiggen JA;
XX WPI; 1998-437449/37.
XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
XX growth factor receptor, useful for inhibiting cell proliferation and
XX for treating cancers
XX Claim 5; Page 78; 109pp; English.
XX The present invention describes enzymatic nucleic acid molecules (NAMEs)
XX which specifically cleave RNA derived from an epidermal growth factor
XX receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
XX represent specifically claimed target sequence from human EGF-R. AAV98044
XX to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and

```

CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NAMS can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell.
XX
SQ Sequence 17 BP; 2 A; 1 C; 4 G; 10 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 550 AGTTTTCATTGT 562

Db 5 AGUUUUCAUGU 17

RESULT 452

AAV97735
ID AAV97735 standard; RNA; 17 BP.

XX AAV97735;

DT 17-MAR-1999 (first entry)

DE Human EGF-R target sequence nucleotide position 4157.

XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
XX cancer; genetic drift; detection; mutation; ss.

OS Homo sapiens.

XX WO9833893-A2.

PD 06-AUG-1998.

PF 14-JAN-1998; 98WO-US00730.

XX 04-DEC-1997; 97US-0985162.

PR 31-JAN-1997; 97US-0036476.

XX (RIBO-) RIBOZYME PHARM INC.

PA (UYAS-) UNIV ASTON.

XX Akhtar S, Fell P, McSwiggen JA;

XX WPI; 1998-437449/37.

XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and
PT for treating cancers

XX Claim 5; Page 78; 109pp; English.

XX The present invention describes enzymatic nucleic acid molecules (NAMS)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NAMS can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell.

XX Sequence 17 BP; 2 A; 2 C; 4 G; 9 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 550 AGTTTTCATTGT 562

Db 4 AGUUUUCAUGU 16

RESULT 453

AAV97736

ID AAV97736 standard; RNA; 17 BP.

XX AAV97736;

DT 17-MAR-1999 (first entry)

DE Human EGF-R target sequence nucleotide position 4158.

XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
XX cancer; genetic drift; detection; mutation; ss.

OS Homo sapiens.

XX WO9833893-A2.

PD 06-AUG-1998.

PF 14-JAN-1998; 98WO-US00730.

XX 04-DEC-1997; 97US-0985162.

PR 31-JAN-1997; 97US-0036476.

XX (RIBO-) RIBOZYME PHARM INC.

PA (UYAS-) UNIV ASTON.

XX Akhtar S, Fell P, McSwiggen JA;

XX WPI; 1998-437449/37.

XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and
PT for treating cancers

XX Claim 5; Page 78; 109pp; English.

XX The present invention describes enzymatic nucleic acid molecules (NAMS)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NAMS can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell.

XX Sequence 17 BP; 2 A; 2 C; 5 G; 8 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 550 AGTTTTCATTGT 562

Db 3 AGUUUUCAUGU 15

RESULT 454

AAV97737

ID AAV97737 standard; RNA; 17 BP.

XX AAV97737;

XX

DT 17-MAR-1999 (first entry)
 DE Human EGF-R target sequence nucleotide position 4159.
 XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 XX Homo sapiens.
 XX W09833893-A2.
 XX 06-AUG-1998.
 XX 14-JAN-1998; 98WO-US00730.
 XX 04-DEC-1997; 97US-0985162.
 XX 31-JAN-1997; 97US-0036476.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (UYAS-) UNIV ASTON.
 PI Akhtar S, Fell P, McSwiggen JA;
 DR WPI; 1998-437449/37.
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and
 PT for treating cancers
 XX Claim 5; Page 78; 109pp; English.
 XX The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell.
 XX Sequence 17 BP; 2 A; 3 C; 4 G; 8 U; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 38.5%; Pred. No. 3.9e+02;
 Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 OY 550 AGTTTTCATGCT 562
 DB ||:::||||:::
 2 AGUUUUAUUGU 14
 RESULT 455
 AAA22686
 ID AAA22686 standard; RNA; 17 BP.
 AC AAA22686;
 XX 19-JUN-2000 (first entry)
 DT Integrin subunit beta 3 substrate sequence SEQ ID NO:5912.
 DE Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;

KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 XX W09950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 DR Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 XX Claim 54; Page 236; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 3 A; 0 C; 1 G; 13 U; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 23.1%; Pred. No. 3.9e+02;
 Matches 3; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 OY 1144 TTATTTTATTTTA 1156
 DB ::||:::||||:::
 5 UUAUUUUAUUGUA 17
 RESULT 456
 AAA22687
 ID AAA22687 standard; RNA; 17 BP.
 AC AAA22687;
 XX 19-JUN-2000 (first entry)
 DT Integrin subunit beta 3 substrate sequence SEQ ID NO:5913.
 DE Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;

KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX WO9950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US06507.
 PF
 XX 27-MAR-1998; 98US-0079678.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 PT
 XX Claim 54; Page 236; 305pp; English.
 PS
 XX The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17560 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17623 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
 CC corresponding target sequences; AAA17685 to AAA18386 to AAA19086
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 13 U; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 23.1%; Pred. No. 3.9e+02;
 Matches 3; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1144 TTATTTTATTTTA 1156
 Db 4 UUAUUUUUUUUUA 16
 RESULT 457
 AAA22688
 ID AAA22688 standard; RNA; 17 BP.
 XX
 AC AAA22688;
 XX
 DT 19-JUN-2000 (first entry)
 XX

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5914.
 XX Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX WO9950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US06507.
 PF
 XX 27-MAR-1998; 98US-0079678.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 PT
 XX Claim 54; Page 236; 305pp; English.
 PS
 XX The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17560 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17623 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
 CC corresponding target sequences; AAA17685 to AAA18386 to AAA19086
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 13 U; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 23.1%; Pred. No. 3.9e+02;
 Matches 3; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1144 TTATTTTATTTTA 1156
 Db 3 UUAUUUUUUUUUA 15
 RESULT 458
 AAA22689
 ID AAA22689 standard; RNA; 17 BP.

XX AAAA22689;
 XX 19-JUN-2000 (first entry)
 XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5915.
 XX
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 XX tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
 XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPT; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 236; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 4 A; 0 C; 1 G; 12 U; 0 other;

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Query Match      1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 23.1%; Pred. NO. 3.9e+02;
Matches 3; Conservative 10; Mismatches 0; Indels 0; Gaps 0
QY      1144 TTATTTTATTTTA 1156
          .:|:::|:::|
Db       2 UUAUUUUUUUA 14

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RESULT 459
 AAAA22806/c
 ID AAAA22806 standard; RNA; 17 BP.
 XX
 AC AAAA22806;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6032.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogen
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arth
 KW age related macular degeneration; inflammation; neovascular glau
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; es;
 XX
 OS Homo sapiens.
 XX
 FN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, MCSwigen JA;
 XX
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 243; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules
 CC RNA cleaving activity, which specifically cleave RNA encoded by
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16777
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences f
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent thei
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA1908
 CC and AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to
 CC and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500
 CC AAA21596 to AAA21688 represent their corresponding target sequen
 CC AAA21689 to AAA22475 and AAA223263 to AAA23342 represent ribozyme
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343
 CC AAA23422 represent their corresponding target sequences. The rib
 CC the invention are used for modulating the synthesis, expression
 CC stability of an mRNA encoding angiogenic factor, especially ARNT
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. The
 CC especially used to treat cancer, diabetic retinopathy, age relat
 CC macular degeneration (ARMD), inflammation, and arthritis, as well
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vul
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syn
 CC and other syndromes and diseases related to the levels of ARNT,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 3 G; 14 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1208 AACAAACAAACAA 1220
17 AACAAACAAACAA 5

Db

RESULT 460
AAA22811/c
ID AAA22811 standard; RNA; 17 BP.
XX
AC AAA22811;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6037.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; anti-inflammatory; antiarthritic; antiproliferative; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US06507.
XX
XX 27-MAR-1998; 98US-0079678.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or
XX stability of an mRNA encoding an angiogenic factors
XX
XX Claim 54; Page 244; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with
RNA cleaving activity, which specifically cleave RNA encoded by an aryl
hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
and AA17168 to AA17560 and AA17623 to AA17684 represent their
corresponding target sequences; AA17685 to AA18385 and AA19087 to
AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
and AA19155 to AA19222 represent their corresponding target sequences;
AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
AA21596 to AA21688 represent their corresponding target sequences;
AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences
for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
AA23422 represent their corresponding target sequences. The ribozymes of
the invention are used for modulating the synthesis, expression and/or
stability of an mRNA encoding angiogenic factor, especially ARNT,
integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
especially used to treat cancer, diabetic retinopathy, age related
macular degeneration (ARMD), inflammation, and arthritis, as well as
neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
and other syndromes and diseases related to the levels of ARNT, Tie-2,
integrin subunit alpha-6, or integrin subunit beta-3.

XX
SQ Sequence 17 BP; 1 A; 0 C; 5 G; 11 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 AACAAACAAACAA 1219
13 AACAAACAAACAA 1

Db

RESULT 461
AAV93569
ID AAV93569 standard; RNA; 17 BP.
XX
AC AAV93569;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human B-raf substrate nucleotide position 1724.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene;
KW delivery; screening; identification; synthesis; deprotection;
KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
KW infection; Genetic drift; restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
XX WO9850530-A2.
XX
XX 12-NOV-1998.
XX
XX 05-MAY-1998; 98WO-US09249.
XX
XX 19-DEC-1997; 97US-0068212.
XX
XX 09-MAY-1997; 97US-0046059.
XX
XX 09-JUN-1997; 97US-0049002.
XX
XX 03-JUL-1997; 97US-0051718.
XX
XX 22-AUG-1997; 97US-0056808.
XX
XX 02-OCT-1997; 97US-0061321.
XX
XX 02-OCT-1997; 97US-0061324.
XX
XX 05-NOV-1997; 97US-0064866.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
XX Karpelsky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
XX Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected
XX processes - especially ribozymes that cleave Raf RNA for treating
XX cancer, restenosis, and also new ribozymes and modified nucleoside
XX triphosphates used as antiviral agents and synthons
XX
XX Claim 177; Page 170; 259pp; English.

A method has been developed for the identification of a nucleic acid
capable of modulating a process in a biological system. The method
comprises: (a) introducing into the system a random library of nucleic
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
a random sequence, and a catalytic domain (CD); and (b) identifying NAC
in systems where modulation has occurred and/or determining the sequence
of at least part of the SBDs in such systems. Nucleic acid molecules
with endonuclease activity and catalytic activity, from the present
invention, are used to modulate gene expression in plant and mammalian
cells and to cleave target nucleic acid, particularly for treating
systemic diseases caused by specific RNA, e.g. cancer, inflammation,
psoriasis, non-hepatic ascites and infection. They may also be used to
detect genetic drift and mutations in diseased cells and to determine

CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.

XX SQ Sequence 17 BP; 6 A; 2 C; 3 G; 6 U; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 69.2%; Pred. No. 3.9e+02;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 656 TAGATATGCAAG 669
 Db 4 UAGAUUUGCAAG 16

RESULT 462
 AAV93570
 ID AAV93570 standard; RNA; 17 BP.
 XX AC AAV93570;
 XX DT 16-FEB-1999 (first entry)
 XX DE Human B-raf substrate nucleotide position 1726.

XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.

OS Homo sapiens.
 XX PN WO9850530-A2.
 XX PD 12-NOV-1998.
 XX PF 05-MAY-1998; 98WO-US09249.
 XX PR 19-DEC-1997; 97US-0068212.
 XX PR 09-MAY-1997; 97US-0046059.
 XX PR 09-JUN-1997; 97US-0049002.
 XX PR 03-JUL-1997; 97US-0051718.
 XX PR 22-AUG-1997; 97US-0056808.
 XX PR 02-OCT-1997; 97US-0061321.
 XX PR 02-OCT-1997; 97US-0061324.
 XX PR 05-NOV-1997; 97US-0064866.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
 PI Karpelsky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
 XX WPI; 1999-009494/01.

XX PT Identifying new catalytic nucleic acid that modulates selected
 PT processes - especially ribozymes that cleave Raf RNA for treating
 PT cancer, restenosis, and also new ribozymes and modified nucleoside
 PT triphosphates used as antiviral agents and synthons

XX PS Claim 177; Page 170; 259pp; English.

XX CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence

CC of at least part of the SBDs in such systems. Nucleic acid molecules
 CC with endonuclease activity and catalytic activity, from the present
 CC invention, are used to modulate gene expression in plant and mammalian
 CC cells and to cleave target nucleic acid, particularly for treating
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
 CC psoriasis, non-hepatic ascites and infection. They may also be used to
 CC detect genetic drift and mutations in diseased cells and to determine
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.

XX SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 U; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 69.2%; Pred. No. 3.9e+02;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 656 TAGATATGCAAG 668
 Db 2 UAGAUUUGCAAG 14

RESULT 463
 AAF03149/C
 ID AAF03149 standard; DNA; 17 BP.
 XX AC AAF03149;
 XX DT 16-FEB-2001 (first entry)
 XX DE Hammerhead ribozyme substrate #1444.

XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.
 XX PN WO200061729-A2.
 XX PD 19-OCT-2000.
 XX PF 11-APR-2000; 2000WO-US09721.
 XX PR 12-APR-1999; 99US-0129390.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.

XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -

XX PS Claim 37; Page 88; 164pp; English.

XX CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.

XX SQ Sequence 17 BP; 4 A; 5 C; 0 G; 8 T; 0 other;
 Query Match 1.0%; Score 13; DB 1; Length 17;

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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1587 TCGAATATATAAAA 1599
      |||||
      17 TCGAATATATAAAA 5

Db

RESULT 464
AAAF03150/c
ID      AAFA03150 standard; DNA; 17 BP.
XX
XX
AC      AAFA03150;
XX
XX      16-FEB-2001 (first entry)
XX
XX      Hammerhead ribozyme substrate #1445.
XX
XX      Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX      interferon alpha; ss.
XX
XX      Homo sapiens.
XX
XX      MO200061729-A2.
XX
XX      19-OCT-2000.
XX
XX      11-APR-2000; 200WO-US09721.
XX
XX      12-APR-1999; 99US-0129390.
XX
XX      (RIBO-) RIBOZYME PHARM INC.
XX
XX      Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
XX      WPI; 2000-647423/62.
XX
XX      Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX      useful for producing e.g. granulocyte colony stimulating factor
XX      protein, interferon alpha and erythropoietin -
XX
XX      Claim 37; Page 88; 164pp; English.
XX
XX      The present invention relates to enzymatic and antisense nucleic acid
XX      molecules that act as inhibitors of the expression of repressor genes
XX      encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX      transcription factor gene, IRF-2 and/or the C/EBP Displacement
XX      Protein (CDP). Inhibition of the repressors removes prevents
XX      inhibition (and consequently increases expression of) genes involved in
XX      the production of erythropoietin, granulocyte colony stimulating factor
XX      protein and interferon alpha.
XX
XX      Sequence 17 BP; 5 A; 3 C; 0 G; 9 T; 0 other;

Query Match      1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1587 TCGAATATATAAAA 1599
      |||||
      15 TCGAATATATAAAA 3

Db

RESULT 465
AAAF03151/c
ID      AAFA03151 standard; DNA; 17 BP.
XX
XX
AC      AAFA03151;
XX
XX      16-FEB-2001 (first entry)
XX
XX      Hammerhead ribozyme substrate #1446.
XX

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XX 27-MAR-2000; 2000US-192176P.
PR 27-MAR-2000; 2000US-192176P.
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX
XX Claim 7; Page 149; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalasassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention.
XX
XX Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 AAGATTCTCTGGTT 522
XX |||||
XX Db 17 AAGATTCTCTGGTT 5
XX
XX RESULT 467
XX ABA78929
XX ID ABA78929 standard; DNA; 17 BP.
XX
XX AC ABA78929;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE Factor V mutation correcting oligonucleotide SEQ ID NO: 1775.
XX
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalasassaemia; haemoglobin alpha locus 1; MLH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antileptic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200173002-A2.
XX
XX PD 04-OCT-2001.

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PF 27-MAR-2001; 2001WO-US09761.
XX
XX 27-MAR-2000; 2000US-192176P.
PR 27-MAR-2000; 2000US-192179P.
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX
XX Claim 7; Page 149; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalasassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention.
XX
XX Sequence 17 BP; 3 A; 3 C; 3 G; 8 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 AAGATTCTCTGGTT 522
XX |||||
XX Db 1 AAGATTCTCTGGTT 13
XX
XX RESULT 468
XX ABA78932/c
XX ID ABA78932 standard; DNA; 17 BP.
XX
XX AC ABA78932;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE Factor V mutation correcting oligonucleotide SEQ ID NO: 1778.
XX
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalasassaemia; haemoglobin alpha locus 1; MLH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antileptic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200173002-A2.
XX
XX PD 04-OCT-2001.

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XX 27-MAR-2001; 2001WO-US09761.
XX
XX 27-MAR-2000; 2000US-192176P.
XX
XX 27-MAR-2000; 2000US-192179P.
XX
XX 01-JUN-2000; 2000US-208538P.
XX
XX 30-OCT-2000; 2000US-244989P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX
XX Claim 7; Page 149; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), presenilin-1 (PSEN1) and
XX (UGT1) amyloid precursor protein (APC). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention.
XX
XX Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 510 AAGATTCTCTGGTT 522
DB |||||
16 AAGATTCTCTGGTT 4
XX
RESULT 469
ABA78933
ID ABA78933 standard; DNA; 17 BP.
XX
XX ABA78933;
XX
XX 24-JAN-2002 (first entry)
XX
XX Factor V mutation correcting oligonucleotide SEQ ID NO: 1779.
XX
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; actinase;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytosstatic; antisickling; antianaemic; haemostatic;
XX antilipemic; ss.
XX
XX Homo sapiens.
XX
XX WO200173002-A2.
XX

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PD 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-US09761.
XX
XX 27-MAR-2000; 2000US-192176P.
XX
XX 27-MAR-2000; 2000US-192179P.
XX
XX 01-JUN-2000; 2000US-208538P.
XX
XX 30-OCT-2000; 2000US-244989P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX
XX Claim 7; Page 149; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), presenilin-1 (PSEN1) and
XX (UGT1) amyloid precursor protein (APC). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention.
XX
XX Sequence 17 BP; 3 A; 3 C; 3 G; 8 T; 0 other;
XX
Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 510 AAGATTCTCTGGTT 522
DB |||||
2 AAGATTCTCTGGTT 14
XX
RESULT 470
ABK56156/c
ID ABK56156 standard; RNA; 17 BP.
XX
XX ABK56156;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human CLCA1 gene enzymatic nucleic acid #527.
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX acetylcysteine.
XX
XX Homo sapiens.
XX
XX WO200211674-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US24970.
XX

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PR 09-AUG-2000; 2000US-224383P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTAX USA LLC.
 PA (THOM/) THOMPSON J.
 XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX WPI; 2002-217145/27.
 DR Enzymatic polynucleotide that down regulates expression of chloride
 XX channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 XX Claim 4; Page 62; 152pp; English.
 PS The invention relates to enzymatic nucleic acid molecules that down
 XX regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX Sequence 17 BP; 12 A; 0 C; 1 G; 4 U; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1142 ATTTATTTATTT 1154
 DB |||||||
 17 ATTTATTTATTT 5
 RESULT 471
 ABK57482/c
 ID ABK57482 standard; RNA; 17 BP.
 AC ABK57482;
 XX 02-JUL-2002 (first entry)
 DT Human CLCA1 gene enzymatic nucleic acid #1853.
 DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 XX acetylcysteine.
 XX Homo sapiens.
 OS WO200211674-A2.
 XX 14-FEB-2002.
 PD 09-AUG-2001; 2001WO-US24970.
 XX 09-AUG-2000; 2000US-224383P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTAX USA LLC.
 PA (THOM/) THOMPSON J.
 XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX WPI; 2002-217145/27.
 DR Enzymatic polynucleotide that down regulates expression of chloride
 XX channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 XX Claim 4; Page 62; 152pp; English.
 PS The invention relates to enzymatic nucleic acid molecules that down
 XX regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX Sequence 17 BP; 12 A; 0 C; 1 G; 4 U; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1142 ATTTATTTATTT 1154
 DB |||||||
 17 ATTTATTTATTT 5

PA (SYNT) SYNTAX USA LLC.
 FA (THOM/) THOMPSON J.
 XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX WPI; 2002-217145/27.
 DR Enzymatic polynucleotide that down regulates expression of chloride
 XX channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 XX Claim 4; Page 114; 152pp; English.
 PS The invention relates to enzymatic nucleic acid molecules that down
 XX regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX Sequence 17 BP; 11 A; 1 C; 0 G; 5 U; 0 other;
 SQ Query Match 1.0%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1142 ATTTATTTATTT 1154
 DB |||||||
 14 ATTTATTTATTT 2
 RESULT 472
 ABN07606
 ID ABN07606 standard; DNA; 17 BP.
 AC ABN07606;
 XX 29-MAY-2002 (first entry)
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7598.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; bGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; ampicillin; screening; ss.
 XX Homo sapiens.
 OS WO200192524-A2.
 XX 06-DEC-2001.
 PD 25-MAY-2001; 2001WO-US16981.
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.

PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US000670.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 7598; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 939 GCCACCATCTTAC 951
Db 5 GCCACCATCTTAC 17
RESULT 473
ABN07612
ID ABN07612 standard; DNA; 17 BP.
XX AC ABN07612;
XX 29-MAY-2002 (first entry)
DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7604.
DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS
XX W0200192524-A2.
PN

06-DEC-2001.
25-MAY-2001; 2001WO-US16981.
26-MAY-2000; 2000US-207456P.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 7604; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 other;
SQ
Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 941 CACCATCTTACTT 953
Db 1 CACCATCTTACTT 13
RESULT 474
ABKL7633/C
ID ABKL7633 standard; RNA; 17 BP.
XX

ABK17633;
09-APR-2002 (first entry)
Human ERG hammerhead ribozyme target sequence, Seq ID No 280.
Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
tumour angiogenesis; diabetic retinopathy; macular degeneration;
neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
angiofibroma of tuberosus sclerolosis; port-wine stain; wound healing;
Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
amberzyme.
Homo sapiens.
WO200108124-A2.
22-NOV-2001.
16-MAY-2001; 2001WO-US15866.
16-MAY-2000; 2000US-0572021.
(RIBO-) RIBOZYME PHARM INC.
(GLAX) GLAXO GROUP LTD.
Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
WPI; 2002-082995/11.
Novel polynucleotide which down regulates expression of Ets-related
gene, useful for treating cancer, diabetic retinopathy, macular
degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
syndrome -
Claim 4; Page 63; 149pp; English.
The invention relates to a nucleic acid molecule (I) which down regulates
expression of an Ets-related gene (ERG). (I) is useful for treating
conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
tumour angiogenesis, diabetic retinopathy, macular degeneration,
neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
vulgaris, angiofibroma of tuberosus sclerolosis, port-wine stains, Sturge
Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
treating a patient having a condition associated with the level of ERG,
by contacting cells of the patient with (I) under conditions suitable for
the treatment. The method comprises the use of one or more therapies
under conditions suitable for the treatment. Leukaemia or tumour
angiogenesis is treated by administering (I) to the patient in
conjunction with one or more of other therapies such as radiation or
chemotherapy treatment. (I) is useful for reducing ERG activity in a
cell, by contacting the cell with RNA. (I) is useful for cleaving RNA of
ERG gene, by contacting the cell with RNA, in the presence of a divalent
cation such as Mg2+. (I) is useful for diagnosis of conditions and
diseases related to the expression of ERG, and as diagnostic tool to
examine genetic drift and mutations within diseased cells or to detect
the presence of ERG RNA in a cell. (I) is useful for specifically
targeting genes that share homology with ERG gene or ERG fusion genes.
ABK17354-ABK22719 represent nucleic acids, including antisense and
enzymatic nucleic acid molecules which regulate expression of ERG, and
related PCR primers of the invention.

DB
14 ATTTTAAATACA 2
RESULT 475
ABK34689
ID ABE34689 standard; DNA; 17 BP.
XX
AC ABE34689;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 326.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PP 17-SEP-2002; 2002WO-IB04208.
XX
PR 17-SEP-2001; 2001FR-0011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases
associated with tumors and cell degeneration, also related
polypeptides, antibodies and transfected cells -
XX
PS Disclosure; Page 72; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15
consecutive nucleotides from the 17 mer sequence, a sequence with, after
optimal alignment, at least 80 % identity to the 17 mer sequence, a
sequence that hybridizes to them under highly stringent conditions, or
the complement of any of them, or the corresponding RNA. The novel
isolated nucleic acids of the invention are useful as probes and primers
for detecting, identifying, quantifying and/or amplifying a nucleic acid,
e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
and for production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterised by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 7 A; 1 C; 5 G; 4 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 419 ATCAGTGAAGATG 431
DB 2 ATCAGTGAAGATG 14

RESULT 476
AAAX79107/c
ID AAX79107 standard; DNA; 18 BP.
XX AC AAX79107;
XX DT 17-AUG-1999 (first entry)
XX DE Primer NGA63-F for A.thaliana SSLP marker.
XX MSH6; MutS homologue; plant; DNA mismatch repair; genetic variation;
KW characteristic; microsatellite; primer; PCR; amplification; SSLP; ss;
KW simple sequence length polymorphism.
XX OS Synthetic.
OS Arabidopsis thaliana.
XX WO9919492-A2.
XX PN 22-APR-1999.
XX PD 09-OCT-1998; 98WO-EP06977.
XX PF 10-OCT-1997; 97AU-0009745.
XX PR (RHON) RHONE-POULENC AGROCHIMIZ.
XX PA Betzner AS, Doutriaux M, Freyssinet G, Perez P;
XX PI WPI; 1999-277644/23.
XX DR DNA encoding protein functionally involved in the DNA mismatch
PT repair system of a plant
XX Example 3; Page 26; 117pp; English.
XX The invention relates to the isolation of the Arabidopsis thaliana MSH3
CC (AAX79066) and MSH6 (AAX79067) genes. These genes are MutS homologues
CC (MSH) from plants and are involved in DNA mismatch repair. The DNA
CC sequence can be used in processes for at least partially inactivating a
CC DNA mismatch repair system of a plant, for increasing genetic variation
CC in a plant, and for obtaining a plant with a desired characteristic.
CC Primers AAX79105-X79160 represent 28 primer pairs used to amplify short
CC allelic repeat fragments designated Simple Sequence Length Polymorphisms
CC (SSLP). These fragments can be used as markers in the analysis of
CC homologous recombination between genomes of A.thaliana subspecies.
XX SQ Sequence 18 BP; 8 A; 5 C; 5 G; 0 U; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 895 CTGTGCGCTTGTT 907
DB 13 CTGTGCGCTTGTT 1
RESULT 477
AAZ95455/c
ID AAZ95455 standard; cDNA; 18 BP.
XX AC AAZ95455;
XX DT 01-JUN-2000 (first entry)
XX DE TEIL random binding site selection oligonucleotide #73.
XX Tobacco; ethylene insensitive 3; TEIL; transcription factor; plant;
KW regulation; ethylene inducible gene; environmental stress; resistance;
KW ss.

XX WPI; 2001-418275/44.
 XX Novel mRNA binding motif that is capable of binding and destabilizing
 PT the mRNA, useful as an immunogen to generate anti-mRNA binding motif
 PT antibodies which are useful for diagnostic purposes -
 XX
 XX Example 1; Fig 3; 87pp; English.
 XX
 XX The invention provides a messenger ribonucleic acid (mRNA) binding motif
 CC that is capable of binding and destabilising the mRNA. The mRNA binding
 CC motif is useful as an immunogen to generate antibodies, which are useful
 CC as standards in assays for the motif ligand, for detecting the motif
 CC ligand in clinical samples for diagnostic purposes, and for in vivo
 CC imaging. A polypeptide that is specifically co-precipitated by the
 CC antibody is useful for effecting a number of interventions into cell
 CC growth and proliferation. Sequences AAH22857-66 represent sense and
 CC antisense DNA oligomers specific for epidermal growth factor receptor
 CC (EGF-R), used in RNA electrophoretic gel mobility shift assay (REMSA).
 XX
 XX Sequence 18 BP; 2 A; 3 C; 5 G; 8 T; 0 other;
 SQ

Query Match 1.0%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 550 AGTTTTCATTGT 562
 |||||
 Db 3 AGTTTTCATTGT 15

RESULT 479
 AAH22864/C
 ID AAH22864 standard; DNA; 18 BP.
 XX
 AC AAH22864;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE EGF-R mRNA specific oligomer EGF-23a.as.
 XX
 XX Messenger ribonucleic acid; mRNA binding motif; immunogen; cell growth;
 KW Grb7; epidermal growth factor receptor; EGF-R; REMSA; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200148193-A1.
 PN
 PD 05-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-AU01595.
 XX
 PR 23-DEC-1999; 99AU-0004835.
 XX
 XX (UTWA-) UNIV WESTERN AUSTRALIA.
 XX
 XX Leedman PJ, Balmer L, Thomson A;
 XX
 XX WPI; 2001-418275/44.
 XX
 XX Novel mRNA binding motif that is capable of binding and destabilizing
 PT the mRNA, useful as an immunogen to generate anti-mRNA binding motif
 PT antibodies which are useful for diagnostic purposes -
 XX
 XX Example 1; Fig 3; 87pp; English.
 XX
 XX The invention provides a messenger ribonucleic acid (mRNA) binding motif
 CC that is capable of binding and destabilising the mRNA. The mRNA binding
 CC motif is useful as an immunogen to generate antibodies, which are useful
 CC as standards in assays for the motif ligand, for detecting the motif
 CC ligand in clinical samples for diagnostic purposes, and for in vivo
 CC imaging. A polypeptide that is specifically co-precipitated by the
 CC antibody is useful for effecting a number of interventions into cell

CC growth and proliferation. Sequences AAH22857-66 represent sense and
 CC antisense DNA oligomers specific for epidermal growth factor receptor
 CC (EGF-R), used in RNA electrophoretic gel mobility shift assay (REMSA).
 XX
 XX Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 other;
 SQ

Query Match 1.0%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 550 AGTTTTCATTGT 562
 |||||
 Db 16 AGTTTTCATTGT 4

RESULT 480
 AAH22864/C
 ID AAH22864 standard; DNA; 18 BP.
 XX
 AC AAH22864;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Human genetic marker PCR primer SEQ ID NO: 29.
 XX
 XX Genetic marker; genetic disease diagnosis; cystic fibrosis; haemophilia;
 KW sickle cell disease; muscular dystrophy; Huntington's disease;
 KW retinoblastoma; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200134839-A1.
 PN
 PD 17-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30493.
 XX
 PR 12-NOV-1999; 99US-0165301.
 XX
 XX (DUNL/) DUNLOP C L M.
 XX (WEIS/) WEISEL J M.
 XX
 XX Dunlop CLM, Weisel JM;
 XX
 XX WPI; 2001-329096/34.
 XX
 XX Detecting multiple genetic markers in one assay, useful to
 PT simultaneously detect a number of genetic disorders, comprises
 PT generating extension products and separating them on the basis of
 PT melting behavior is -
 XX
 XX Claim 44; Page 33; 40pp; English.
 XX
 XX The present invention describes a method of identifying the presence of a
 CC plurality of genetic markers in a subject, involving generating extension
 CC products using PCR primers flanking the plurality of markers, separating
 CC the extension products depending on their melting temperatures, and
 CC analysing them to determine the presence or absence of each genetic
 CC marker. This can be used in the diagnosis of genetic diseases, including
 CC familial hypercholesterolaemia, cystic fibrosis, Tay-Sachs, thalassaemia,
 CC sickle cell disease, phenylketonuria, galactosaemia, fragile X syndrome,
 CC haemophilia A, myotonic dystrophy, medium chain acyl-CoA dehydrogenase,
 CC maturity onset diabetes, cystinuria, methylomalic aciduria, urea cycle
 CC disorders, hereditary fructose intolerance, hereditary haemochromatosis,
 CC neonatal thrombocytopenia, Gaucher's disease, tyrosinaemia, Wilson's
 CC disease, acaptonuria, hypolactasia, Baker's disease, argininaemia,
 CC adenomatous polyposis coli, hereditary nonpolyposis colorectal cancer,
 CC Huntington's disease, adult polycystic kidney disease,
 CC alpha-1-antitrypsin deficiency, Duchenne muscular dystrophy, Marfan's
 CC syndrome, neurofibromatosis, osteogenesis imperfecta, retinoblastoma,
 CC Friedreich's ataxia, haemoglobinopathies, Leber's hereditary optic
 CC neuropathy, MCAD, Canavan's disease, retinitis pigmentosa, Bloom
 CC syndrome, Fanconi anaemia or Neimann Pick disease. The present sequence

```

CC is one of the PCR primers of the invention.
XX
SQ Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 799 TGCCTAATAGTCA 811
DB 14 TGCCTAATAGTCA 2

RESULT 481
AAF87476
ID AAF87476 standard; DNA; 18 BP.
XX
AC AAF87476;
XX
XX 09-JUL-2001 (first entry)
XX
XX Corynebacterium thermoaminogenes icd primer.
XX
XX Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
XX thermotolerant; aceA; accBC; dter2; pfk; scrB; gluABCD;
XX pdhA; pc; ppc; acn; icd; lpd; odhA; PCR primer; ss.
XX
XX Corynebacterium thermoaminogenes.
XX
XX WO200125447-A1.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000WO-JP06913.
XX
XX 04-OCT-1999; 99JP-0282716.
XX 01-NOV-1999; 99JP-0311147.
XX 21-APR-2000; 2000JP-0120687.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Kimura E;
XX Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
XX Sugimoto S;
XX
XX WPI; 2001-300170/31.
XX
XX Proteins and their DNA useful for microbial production of L-amino acids
XX
XX Example 1; Page 28; 215pp; Japanese.
XX
XX The present sequence is provided in a specification relating to genes
XX encoding thermophilic amino acid biosynthesis system enzymes of
XX the thermotolerant bacterium Corynebacterium thermoaminogenes.
XX The novel proteins retain at least 30% isocitrate ligase activity
XX after heating at 500C for 5 minutes. DNA fragments encoding the
XX enzymes were isolated from a Corynebacterium thermoaminogenes
XX chromosomal DNA plasmid library by PCR. The DNA may be used for
XX developing strains of amino acid producing microorganisms.
XX
XX Sequence 18 BP; 2 A; 2 C; 2 G; 7 T; 0 other;
XX
XX Proteins and their DNA useful for microbial production of L-amino acids
XX
XX Example 1; Page 28; 215pp; Japanese.
XX
XX The present sequence is provided in a specification relating to genes
XX encoding thermophilic amino acid biosynthesis system enzymes of
XX the thermotolerant bacterium Corynebacterium thermoaminogenes.
XX The novel proteins retain at least 30% isocitrate ligase activity
XX after heating at 500C for 5 minutes. DNA fragments encoding the
XX enzymes were isolated from a Corynebacterium thermoaminogenes
XX chromosomal DNA plasmid library by PCR. The DNA may be used for
XX developing strains of amino acid producing microorganisms.
XX
XX Sequence 18 BP; 2 A; 2 C; 2 G; 7 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 883 GTCCTTGTTCCAC 895
DB 3 GTCCTTGTTCCAC 15

RESULT 482
AAF87476
ID AAF87476 standard; DNA; 18 BP.
XX
AC AAF87476;
XX
XX 09-JUL-2001 (first entry)
XX
XX Corynebacterium thermoaminogenes icd primer.
XX
XX Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
XX thermotolerant; aceA; accBC; dter2; pfk; scrB; gluABCD;
XX pdhA; pc; ppc; acn; icd; lpd; odhA; PCR primer; ss.
XX
XX Corynebacterium thermoaminogenes.
XX
XX WO200125447-A1.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000WO-JP06913.
XX
XX 04-OCT-1999; 99JP-0282716.
XX 01-NOV-1999; 99JP-0311147.
XX 21-APR-2000; 2000JP-0120687.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Kimura E;
XX Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
XX Sugimoto S;
XX
XX WPI; 2001-300170/31.
XX
XX Proteins and their DNA useful for microbial production of L-amino acids
XX
XX Example 1; Page 28; 215pp; Japanese.
XX
XX The present sequence is provided in a specification relating to genes
XX encoding thermophilic amino acid biosynthesis system enzymes of
XX the thermotolerant bacterium Corynebacterium thermoaminogenes.
XX The novel proteins retain at least 30% isocitrate ligase activity
XX after heating at 500C for 5 minutes. DNA fragments encoding the
XX enzymes were isolated from a Corynebacterium thermoaminogenes
XX chromosomal DNA plasmid library by PCR. The DNA may be used for
XX developing strains of amino acid producing microorganisms.
XX
XX Sequence 18 BP; 2 A; 2 C; 2 G; 7 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 883 GTCCTTGTTCCAC 895
DB 3 GTCCTTGTTCCAC 15

RESULT 482

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```

AAF87482/c
ID AAF87482 standard; DNA; 18 BP.
XX
AC AAF87482;
XX
XX 09-JUL-2001 (first entry)
XX
XX Corynebacterium thermoaminogenes icd primer.
XX
XX Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
XX thermotolerant; aceA; accBC; dter2; pfk; scrB; gluABCD;
XX pdhA; pc; ppc; acn; icd; lpd; odhA; PCR primer; ss.
XX
XX Corynebacterium thermoaminogenes.
XX
XX WO200125447-A1.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000WO-JP06913.
XX
XX 04-OCT-1999; 99JP-0282716.
XX 01-NOV-1999; 99JP-0311147.
XX 21-APR-2000; 2000JP-0120687.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Kimura E;
XX Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
XX Sugimoto S;
XX
XX WPI; 2001-300170/31.
XX
XX Proteins and their DNA useful for microbial production of L-amino acids
XX
XX Example 1; Page 28; 215pp; Japanese.
XX
XX The present sequence is provided in a specification relating to genes
XX encoding thermophilic amino acid biosynthesis system enzymes of
XX the thermotolerant bacterium Corynebacterium thermoaminogenes.
XX The novel proteins retain at least 30% isocitrate ligase activity
XX after heating at 500C for 5 minutes. DNA fragments encoding the
XX enzymes were isolated from a Corynebacterium thermoaminogenes
XX chromosomal DNA plasmid library by PCR. The DNA may be used for
XX developing strains of amino acid producing microorganisms.
XX
XX Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 883 GTCCTTGTTCCAC 895
DB 15 GTCCTTGTTCCAC 3

RESULT 483
ABK85460/c
ID ABK85460 standard; DNA; 18 BP.
XX
AC ABK85460;
XX
XX 16-AUG-2002 (first entry)
XX
XX Shrimp alkaline phosphatase (SAP) cDNA, PCR primer #1.
XX
XX Shrimp; heat labile alkaline phosphatase; SAP; DNA sequencing reaction;
XX cloning vector dephosphorylation; PCR amplification product-mixture;
XX reporter enzyme; PCR; primer; ss.
XX
XX Pandalus borealis.
XX

```

```

OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 6
XX FT /*tag= a
XX FT /mod_base= i
XX
XX WO200231157-A2.
XX
XX 18-APR-2002.
XX
XX 10-OCT-2001; 2001WO-GB04509.
XX
XX 10-OCT-2000; 2000GB-0024827.
XX
XX (NOFI-) NORWEGIAN INST FISHERIES & AQUACULTURE.
XX (GARD/) GARDNER R.
XX
XX Gardner R, Nilsen I, Oeverboe K;
XX WPI; 2002-444182/47.
XX
XX Novel recombinant heat labile shrimp alkaline phosphatase useful in
XX molecular biology techniques, in the production of DNA based
XX therapeutics or in forensic science, and for laboratory protocols
XX
XX Example 3; Page 34; 54pp; English.
XX
XX The present invention relates to the isolation of shrimp (Pandalus
XX borealis) heat labile alkaline phosphatase (E.C. 3.1.3.1) referred
XX to as SAP, and polynucleotide sequences encoding it. The SAP enzyme
XX is useful in the dephosphorylation of cloning vectors prior to
XX ligation reactions, in the treatment of PCR amplification
XX product-mixtures prior to DNA sequencing reactions, in molecular
XX biology techniques, in the production of DNA based therapeutics or
XX in forensic science, for laboratory protocols, and as a reporter
XX enzyme. The SAP enzyme is heat labile and cold active making it
XX particularly suitable for use in multi-step laboratory protocols
XX where a simple heating step deactivates the enzyme. The present
XX sequence represents a SAP PCR primer used in the examples of the
XX present invention.
XX
XX Sequence 18 BP; 7 A; 1 C; 4 G; 2 T; 4 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 18;
XX Best Local Similarity 72.2%; Pred. No. 4.1e+02;
XX Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 896 CTGTGTCACACTGCGCTT 903
XX 18 YTTTTCACATGCGCTT 1
XX
XX RESULT 484
XX AAD31944/c
XX ID AAD31944 standard; DNA; 18 BP.
XX
XX AC AAD31944;
XX
XX 18-JUN-2002 (first entry)
XX
XX Salmonella typhimurium amyloid precursor protein (APP) DNA.
XX
XX Microbial virulence factor; genetic predisposition; Alzheimer's disease;
XX Parkinson's disease; schizophrenia; frontotemporal lobe dementia;
XX hereditary multi-infarct dementia; primary X-linked mental retardation;
XX dementia; myopathy; familial British dementia; psychiatric disorder;
XX transgenic animal; amyloid precursor protein; APP; ds.
XX
XX Salmonella typhimurium.
XX
XX WO200214546-A1.
XX

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PD 21-FEB-2002.
XX
XX 15-FEB-2001; 2001WO-IB00189.
XX
XX 16-AUG-2000; 2000WO-IB01127.
XX
XX (FRIT/) FRITZSCHE M.
XX
XX Fritzsche M;
XX
XX WPI; 2002-241910/29.
XX
XX Use of DNA sequence having fragment of nucleic acid encoding putative
XX microbial virulence factor useful for identification of disease e.g.
XX Alzheimer's disease, caused by mutations or for genetic predisposition
XX
XX Example 1; Page 21; 52pp; English.
XX
XX The present invention relates to the use of a DNA sequence comprising a
XX fragment of a nucleic acid encoding a putative microbial virulence factor
XX for the identification of a disease caused by mutations or for a genetic
XX predisposition. The invention also relates to a method for identification
XX of a disease which comprises detecting the presence of a mutation within
XX a nucleic acid sequence of the fragment of virulence factor in a tissue-
XX or blood sample of a subject, where the tissue sample is a foetal graft
XX for neurotransplantation and where the sequence is inserted in the 3'
XX UTR (untranslated region) of the gene and mutation is found in the
XX polyadenylation signal of G1. The method is useful for identification
XX of a disease caused by mutation or for their genetic predisposition
XX where the disease is human disease which is from Alzheimer's disease,
XX Parkinson's disease, schizophrenia, myopathy, other forms of dementia,
XX (frontotemporal lobe dementia, autosomal dominant Parkinson Lewy-Body
XX dementia, hereditary multi-infarct dementia, familial British dementia,
XX primary X-linked mental retardation) and where the human disease
XX constitutes a predisposition or a genetic variation, the pathological
XX manifestation of which is triggered by medications or drugs which is
XX preferably cannabis, where the manifestation comprises any forms of
XX dementia, schizophrenia or related psychiatric disorders. The invention
XX also relates to transgenic animals (e.g. comprising a non-functional
XX endogenous cannabinoid receptor (CB1) gene) which are useful for the
XX identifying or screening of compounds that have an effect on the
XX activity, expression or regulation of the translated protein (e.g.
XX CB1 protein). The present sequence is Salmonella typhimurium amyloid
XX precursor protein (APP) DNA. This sequence is used in the
XX exemplification of the invention.
XX
XX Sequence 18 BP; 8 A; 2 C; 1 G; 7 T; 0 other;
XX
XX Query Match 1.0%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1050 ATGTATTATTATTA 1062
XX 15 ATGTATTATTATTA 3
XX
XX RESULT 485
XX AAD50202/c
XX ID AAD50202 standard; DNA; 18 BP.
XX
XX AC AAD50202;
XX
XX 24-MAR-2003 (first entry)
XX
XX Human Fragile X gene exon 3 (FragX 3) specific PCR primer #2.
XX
XX Human; cystic fibrosis; Tay-sachs; familial hypercholesterolaemia; FH;
XX fragile X syndrome; haemophilia A; diabetes; cystinuria; tyrosinaemia;
XX urea cycle disorder; hereditary fructose intolerance; Baker's disease;
XX Wilson's disease; alcaptonuria; adult polycystic kidney disease; MCAS;
XX Huntington's disease; myotonic dystrophy; retinitis pigmentosa; cancer;
XX

```

XW Gauchers disease; Canavan's disease; galactosaemia; thrombocytopenia;
KW thalassaemia; sickle cell disease; phenylketonuria; Marfan's syndrome;
KW haemoglobinopathy; Bloom syndrome; Neimann Pick's disease; PCR; primer;
XX Prax3; ss.
OS Homo sapiens.
XX WO200290374-A1.
XX 14-NOV-2002.
PD 06-MAY-2002; 2002WO-US14562.
XX 08-MAY-2001; 2001US-0851501.
XX (AMER-) AMERY GENETICS CORP.
PA Dunlop CLM, Weisel JM;
XX WPI; 2003-103498/09.
DR Identifying the presence or absence of a mutation or polymorphism in a
PT subject, useful for diagnosing genetic diseases, comprises generating
PT extension products and analyzing the melting behavior of the mixed DNA
PT sample -
XX Claim 56; Page 42; 49pp; English.
PS The invention relates to a method for identifying the presence or absence
XX of a mutation or polymorphism in a plurality of genes. The method is used
CC for identifying the presence or absence of a mutation or polymorphism in
CC a subject, or the presence or absence of several genetic markers in a
CC subject for diagnosing genetic diseases, e.g. cystic fibrosis, Tay-sachs,
CC familial hypercholesterolaemia (FH), thalassaemia, sickle cell disease,
CC phenylketonuria, galactosaemia, fragile X syndrome, haemophilia A, onset
CC myotonic dystrophy, medium-chain acyl CoA dehydrogenase, neonatal
CC diabetes, cystinuria, methylmalonic acidemia, urea cycle disorders,
CC hereditary fructose intolerance, hereditary haemochromatosis, neonatal
CC thrombocytopenia, Gauchers disease, tyrosinaemia, Wilson's disease,
CC alcaptonuria, hypolactasia, Baker's disease, argininaemia adenomatous
CC polypsis coli (APC), adult polycystic kidney disease, Duchenne muscular
CC dystrophy, alpha-1-antitrypsin deficiency, hereditary non-polyposis
CC colorectal cancer, Huntington's disease, neurofibromatosis, Marfan's
CC syndrome, osteogenesis imperfecta, retinoblastoma, Freidrich's ataxia,
CC haemoglobinopathies, MCAD, Canavan's disease, Leber's hereditary optic
CC neuropathy, retinitis pigmentosa, Bloom syndrome, Fanconi's anaemia, or
CC Neimann Pick's disease. The present sequence is human fragile X gene
CC exon 3 (fragX 3) specific PCR primer used to illustrate the method of
CC the invention.
XX SQ Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 799 TGCCATAAAGTCA 811
DB 14 TGCCATAAAGTCA 2
RESULT 486
ABZ11062/c
ID ABZ11062 standard; DNA; 18 BP.
XX AC ABZ11062;
XX 16-JAN-2003 (first entry)
XX Haematopoietic cell proliferation disorder related oligonucleotide #1202.
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KW cytosine methylation state; probe; primer; ss.
XX Homo sapiens.
OS Synthetic.
XX WO200277272-A2.
XX 03-OCT-2002.
XX 26-MAR-2002; 2002WO-EP03401.
XX 26-MAR-2001; 2001US-279333P.
XX (EPIG-) EPIGENOMICS AG.
PA Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
PI Lewin A, Lipscher B, Walter S, Model F, Mueller V, Otto T;
PI Pellet C, Schwöpe I, Ziebarth H;
XX WPI; 2003-018942/01.
DR Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent
PT that distinguishes between methylated and non-methylated CpG
PT dinucleotides -
XX Claim 15; Page 78; 117pp; English.
PS The present invention describes a method for detecting and
XX differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related
CC DNA sequences. The nucleotide sequences from the present invention can
CC also be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables
CC a highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients.
XX SQ Sequence 18 BP; 4 A; 0 C; 3 G; 11 T; 0 other;
Query Match 1.0%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1205 TTAACAAACAAA 1217
DB 15 TTAACAAACAAA 3
RESULT 487
ABL46338
ID ABL46338 standard; DNA; 30 BP.
XX AC ABL46338;
XX 26-APR-2002 (first entry)
XX Human interleukin-1 beta oligonucleotide SEQ ID NO:305.
DE

KW Nucleic acid accessible hybridisation site; detection; hybridisation;
 KW characterisation; identification; nucleic acid structure; diagnosis;
 KW PCR primer; probe; ss.

XX Homo sapiens.
 OS Synthetic.

PN WO200198537-A2.

XX 27-DEC-2001.

XX 15-JUN-2001; 2001WO-US19401.

XX 17-JUN-2000; 2000US-212308P.

PR 15-JUN-2001; 2001US-0212308.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichiev V, Allawi H, Dong F, Neri BP, Vener IT;

XX WPI; 2002-049698/06.

XX Identifying oligonucleotides hybridizing to nucleic acids containing
 PT secondary structure, useful in clinical diagnosis, comprises
 PT identifying primers that interact with the target to form an extension
 PT product under amplification conditions -

PS Claim 48; Fig 81A; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides
 CC with desired hybridisation properties to nucleic acid targets containing
 CC secondary structure. The method comprises amplifying a target nucleic
 CC acid having at least one accessible and one inaccessible site. Primers
 CC that form an extension product are identified as the oligonucleotides
 CC which can interact with the folded target nucleic acid. Oligonucleotides
 CC from the present invention can be used in novel detection methods for
 CC clinical diagnostic purposes, including the detection and identification
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 30 BP; 13 A; 4 C; 2 G; 11 T; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 30;

Best Local Similarity 76.2%; Pred. No. 5.6e+02;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1444 CTGGTGAACCTCTTTATTA 1464

DB 1 CTGATGGAATTTATCTAATA 21

RESULT 488

AAZ24085/c

ID AAZ24085 standard; DNA; 16 BP.

XX AAZ24085;

DT 04-FEB-2000 (first entry)

DE N. gonorrhoeae GC3 DNA fragment PCR primer 20.

XX GC3; species-specific detection; amplification; diagnosis; primer; ss.

OS Synthetic.

OS Neisseria gonorrhoeae.

XX DE19918479-A1.

XX 28-OCT-1999.

XX 23-APR-1999; 99DE-1018479.

PR 27-APR-1998; 98US-0067773.

PA (BECT) BECTON DICKINSON & CO.

XX You Q;

XX WPI; 1999-602549/52.

XX Isolated nucleic acid for the GC-3 fragment from Neisseria gonorrhoeae,
 PT useful for species-specific detection -

XX Claim 3; Page 28; 37pp; German.

XX This invention describes a novel isolated nucleic acid (A) for the
 CC Neisseria gonorrhoeae GC-3 sequence. The isolated nucleic acid (A) and
 CC fragments of (A) are used for the species-specific detection of
 CC Neisseria gonorrhoeae in standard amplification or hybridization assays.
 CC Fragments of (A) are species-specific with no detectable cross-reaction
 CC with any other species, so they provide a rapid, reliable and selective
 CC (down to 10 genomic copies) diagnosis. AAZ24068-Z24090 represent PCR
 CC primers used in the identification of the N. gonorrhoeae GC3 fragment
 CC described in the method of the invention.

XX Sequence 16 BP; 5 A; 3 C; 4 G; 4 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 756 TGTATTTGAGCATC 771

DB 16 TGACATTTGAGCATC 1

RESULT 489

AAZ28412/c

ID AAZ28412 standard; DNA; 16 BP.

XX AAZ28412;

XX 20-DEC-1999 (first entry)

DE PCR primer UD28340 used to amplify the D28340 microsatellite marker.

XX PCR primer; microsatellite marker; diagnosis; asthma; predisposition;

XX chromosome 2; genetic polymorphism; D28340; detect; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9950451-A1.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-GE00968.

XX 27-MAR-1998; 98GB-0006652.

XX (ISIS-) ISIS INNOVATION LTD.

XX Cookson WOCM, Moffatt MF, Bhattacharya S, Leaves N;

XX WPI; 1999-601341/51.

XX Diagnosing asthma, or an asthmatic predisposition, from the presence of
 PT specific alleles at a locus on chromosome 2 -

XX Claim 9; Page 8; 21pp; English.

XX PCR primers AAZ28411-Z28412 are used to amplify the microsatellite
 CC markers associated with the allele situated on chromosome 2, containing
 CC the D28340 locus. The D28340 microsatellite markers are contained in the
 CC region of chromosome 2 containing the IL2 (interleukin 2) cluster of

CC genes. The invention relates to a method for diagnosing asthma or a
CC predisposition to asthma. The products of PCR primers AAZ28409-Z28418
CC are used to detect any alleles that may be connected with asthma. The
CC D2S308*3 allele (PCR primers AAZ28409-Z28410 are used to amplify the
CC associated microsatellite markers) is used in the claimed methods to
CC identify children at risk of developing asthma by examination
CC immediately after birth, potentially allowing the disease to be
CC prevented. The methods may also allow a prognosis of the severity of a
CC condition and responses to particular treatments.

XX
SQ Sequence 16 BP; 1 A; 5 C; 3 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 GCAAAATTTGGGCAAG 700
Db 16 GCAAACTGGGCAAG 1
|||||

RESULT 490
AAI67028
ID AAI67028 standard; DNA; 16 BP.
XX
AC AAI67028;
XX
DT 11-FEB-2002 (first entry)
XX
DE Human PLSCL1 intron 5/exon 6 junction sequence.
XX
KW Phospholipid scramblase; PLSCL; membrane protein; virucide; vaccine;
KW cytosolic; leukemia; cancer; PLSCL1; human; ss.
XX
XX Homo sapiens.
XX
XX WO200174295-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10388.
XX
XX 31-MAR-2000; 2000US-193939P.
XX
XX (SCL1) SCRIPPS RES INST.
XX (CLEV-) CLEVELAND CLINIC FOUND.
XX
XX Sims PJ, Silverman RH, Wiedmer T;
XX
XX WPI; 2001-626334/72.
XX
XX Novel membrane proteins, phospholipid scramblase polypeptides, useful
XX for treating and preventing cancer and viral infections, are induced by
XX interferons -
XX
XX Example 8; Page 61; 94pp; English.

XX The invention provides phospholipid scramblase (PLSCL) polypeptides and
XX polynucleotides encoding them. PLSCL are membrane proteins that mediate
XX accelerated trans-bilayer movement of plasma membrane phospholipids in
XX response to elevated cytoplasmic calcium. The PLSCL polypeptides are
XX useful for inhibiting or preventing viral infection (e.g. infection of a
XX membrane-bound virus or virus such as rabdovirus, filovirus, retrovirus,
XX flavivirus, coronavirus, orthomyxovirus, bunyavirus, hepatitis virus,
XX herpesvirus, poxvirus, togavirus, iridovirus, paramyxovirus, arenavirus,
XX HIV, Ebola virus, Marburg virus and Rabies virus). The polynucleotides
XX are useful for treating a subject having or at risk of having a disorder
XX associated with a PLSCL polypeptide or polynucleotide. Compounds
XX modulating the PLSCL activity, are useful for treating viral infection or
XX cancer e.g. hairy cell leukemia, chronic myelogenous leukemia, myeloma,
XX melanoma, renal cell carcinoma, Kaposi's sarcoma, follicular lymphoma,
XX thrombocythemia or erythroleukemia. PLSCL is also useful for treating and
XX preventing cancer. Sequences AAI670194-34 represent human PLSCL1

CC exon/intron junction sequences.

XX Sequence 16 BP; 4 A; 1 C; 2 G; 9 T; 0 other;

SQ

Query Match 1.0%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1196 GTTTTACATTAAACA 1211
Db 1 GTTTTACATTAAACA 16
|||||

RESULT 491
AAD15192
ID AAD15192 standard; DNA; 16 BP.
XX
AC AAD15192;
XX
DT 01-NOV-2001 (first entry)
XX
DE 5' RT-PCR primer for rabbit REC1_22 clone.
XX
XX Fatty lesion development; atherosclerosis; Alzheimer's disease;
XX nervous system disorder; Parkinson's disease; immune system disorder;
XX ischaemia; lymphopenia; leukocyte adhesion deficiency syndrome;
XX haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
XX coagulation disorder; blood platelet disorder; autoimmune disorder;
XX dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
XX Grave's disease; Gene therapy; antiarteriosclerotic; immunostimulant;
XX cardiovascular; antiviral; RT-PCR primer; rabbit; ss.
XX
XX Oryctolagus cuniculus.
XX
XX WO200154651-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02439.
XX
XX 25-JAN-2000; 2000US-0177963.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
XX WPI; 2001-514526/56.
XX
XX New polynucleotides regulated by fatty lesion development and their
XX encoded polypeptides, useful for preventing, treating or ameliorating
XX atherosclerosis, as well as for immune or hyperproliferative disorders
XX
XX Example 2; Page 124; 189pp; English.

XX The present invention relates to an isolated nucleic acid regulated by
XX fatty lesion development, which comprises any of 55 polynucleotide
XX sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
XX antibody is useful for preventing, treating, modulating or ameliorating
XX a medical condition, particularly atherosclerosis. The invention is used
XX as a marker or detector of nervous system disorder or disease (e.g.
XX Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
XX invention may also be useful for treating deficiencies or disorders of
XX the immune system (e.g. lymphopenia, leukocyte adhesion deficiency
XX syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
XX (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
XX coagulation disorders, blood platelet disorders and autoimmune disorders
XX (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
XX The polynucleotide sequence is also used in gene therapy. The present
XX sequence is a 5' RT-PCR primer for rabbit REC1_22 clone.

XX Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;


```

Query Match      1.0%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 897 GTCCTTCGCTTCCTCC 912
DB 1 GGGCCTTCGCTTCCTCC 16

RESULT 492
AAT53752
ID AAT53752 standard; RNA; 17 BP.
XX AC AAT53752;
XX DT 25-MAR-2003 (updated)
XX DT 03-APR-1997 (first entry)
DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2906).
XX KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX KW intercellular adhesion molecule; rel A; tumour necrosis factor;
XX KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX KW translocation; chronic myelogenous leukaemia; CML; cancer;
XX KW Philadelphia chromosome; inflammation; autoimmune disease;
XX KW atherosclerosis; myocardial infarction; stroke; restenosis;
XX KW transplant rejection; rheumatoid arthritis; psoriasis;
XX KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX KW human immunodeficiency virus; acquired immune deficiency syndrome;
XX KW AIDS; ss.
XX OS Rattus rattus.
XX PN W09523225-A2.
XX PD 31-AUG-1995.
XX PP 23-FEB-1995; 95WO-IB00156.
XX PR 30-JAN-1995; 95US-0380734.
XX PR 23-FEB-1994; 94US-0201109.
XX PR 29-MAR-1994; 94US-0218934.
XX PR 04-APR-1994; 94US-0222795.
XX PR 07-APR-1994; 94US-0224483.
XX PR 15-APR-1994; 94US-0227956.
XX PR 15-APR-1994; 94US-0228041.
XX PR 18-MAY-1994; 94US-0245736.
XX PR 06-JUL-1994; 94US-0271280.
XX PR 15-AUG-1994; 94US-0291932.
XX PR 16-AUG-1994; 94US-0291433.
XX PR 17-AUG-1994; 94US-0232620.
XX PR 19-AUG-1994; 94US-0293520.
XX PR 02-SEP-1994; 94US-0300000.
XX PR 08-SEP-1994; 94US-0303039.
XX PR 23-SEP-1994; 94US-0311486.
XX PR 23-SEP-1994; 94US-0311749.
XX PR 28-SEP-1994; 94US-0314397.
XX PR 03-OCT-1994; 94US-0316771.
XX PR 07-OCT-1994; 94US-0319492.
XX PR 11-OCT-1994; 94US-0321993.
XX PR 04-NOV-1994; 94US-0334847.
XX PR 10-NOV-1994; 94US-0337608.
XX PR 28-NOV-1994; 94US-0345516.
XX PR 16-DEC-1994; 94US-0357577.
XX PR 23-DEC-1994; 94US-0363233.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PA Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
XX PI Grimm S, Karpelsky A, Kisich K, Matulic-adamic J, McSwiggen JA;
XX PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
XX PI Thompson JD, Tracz D, Usman N, Wincott FS, Woolf T;

```

```

XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them -
XX for use in inhibiting disease related genes
XX Claim 2; Page 204; 407pp; English.
XX The present sequence represents a preferred target sequence for
XX an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
XX mRNA at the nucleotide base position indicated in the DE line.
XX Regions of the mRNA that do not form secondary folding
XX structures and that contain potential hammerhead and hairpin
XX ribozyme cleavage sites were identified by computer analysis.
XX Ribozymes directed against these mRNA sequences were designed and
XX synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and
XX thereby inhibit ICAM-1 expression, making them useful for reducing
XX transplant rejection and alleviating symptoms in patients with
XX rheumatoid arthritis, asthma and other inflammatory disorders.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 17 BP; 5 A; 0 C; 3 G; 9 U; 0 other;
XX Query Match      1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 31.2%; Pred. No. 4.3e+02;
XX Matches 5; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
QY 1047 TTTATGTATTATTATTA 1062
DB 2 UUGAUGUUAUUA 17

RESULT 493
AAT81507/c
ID AAT81507 standard; RNA; 17 BP.
XX AC AAT81507;
XX DT 14-DEC-1997 (first entry)
XX DE Human c-myb hammerhead ribozyme target sequence (nt. position 2715).
XX KW Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
XX KW smooth muscle cell; hyperproliferation; restenosis; cancer;
XX KW c-myb; coronary angioplasty; ss.
XX OS Homo sapiens.
XX PN W09531541-A2.
XX PD 23-NOV-1995.
XX PP 18-MAY-1995; 95WO-US06368.
XX PR 13-JAN-1995; 95US-0373124.
XX PR 18-MAY-1994; 94US-0245466.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PA Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
XX PI WPI; 1996-010927/01.
XX PT New enzymatic nucleic acid molecules - which cleave RNA produced by
XX e.g. c-myb, for treating restenosis or cancer
XX Claim 1; Page 77; 126pp; English.
XX The present sequence represents the preferred target sequence for an
XX enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
XX the human c-myb sequence at the base position indicated in the
XX descriptor line. The c-myb sequence was screened for optimal ribozyme

```

CC target sites using a computer folding algorithm, and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised and
CC their activities optimised by either varying the length of the binding
CC arms or by modification to prevent degradation by nucleases.
CC The ribozymes cleave the c-myc sequence and can be used to prevent
CC smooth muscle cell hyperproliferation in restenosis, especially after
CC coronary angioplasty, and in cancers.

XX Sequence 17 BP; 7 A; 0 C; 0 G; 10 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1613 ATTAAATATATAATTT 1628

DB 17 AATAAAATATAATTT 2

RESULT 494

AAX71475

ID AAX71475 standard; RNA; 17 BP.

AC AAX71475;

DT 28-JUL-1999 (first entry)

DE Human KDR VEGF receptor hammerhead ribozyme substrate #487.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.

OS Homo sapiens.

PN WO9715662-A2.

PD 01-MAY-1997.

PF 25-OCT-1996; 96WO-US17480.

PR 11-JAN-1996; 96US-0584040.

PR 26-OCT-1995; 95US-0005974.

XX (CHIR) CHIRON CORP.

PA (RIBO-) RIBOZYME PHARM INC.

XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient

XX Claim 4; Page 111; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.

XX Sequence 17 BP; 7 A; 0 C; 4 G; 6 U; 0 other;

RESULT 496

AAX71100

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 4.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1116 GAATAGTTATAAAGAT 1131

DB 2 GGAUAUUUAUAAAGAU 17

RESULT 495

AAX71476

ID AAX71476 standard; RNA; 17 BP.

AC AAX71476;

DT 28-JUL-1999 (first entry)

DE Human KDR VEGF receptor hammerhead ribozyme substrate #488.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.

OS Homo sapiens.

PN WO9715662-A2.

PD 01-MAY-1997.

PF 25-OCT-1996; 96WO-US17480.

PR 11-JAN-1996; 96US-0584040.

PR 26-OCT-1995; 95US-0005974.

XX (CHIR) CHIRON CORP.

PA (RIBO-) RIBOZYME PHARM INC.

XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient

XX Claim 4; Page 111; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.

XX Sequence 17 BP; 7 A; 1 C; 3 G; 6 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 4.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1116 GAATAGTTATAAAGAT 1131

DB 1 GGAUAUUUAUAAAGAU 16

RESULT 496

AAX71100


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PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
XX (CHIR ) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 80; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 3 A; 2 C; 0 G; 12 U; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 4.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1085 ATTTCGAAAAATAGAA 1100
Db ||||| ||||| |||||
17 ATTTCGAAAAATAGAA 2

RESULT 499
AAX69807/C
ID AAX69807 standard; RNA; 17 BP.
XX
XX AAX69807;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1102.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US17480.
XX
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX
XX (CHIR ) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 80; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 3 A; 2 C; 0 G; 12 U; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 4.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1085 ATTTCGAAAAATAGAA 1100
Db ||||| ||||| |||||
17 ATTTCGAAAAATAGAA 2

RESULT 500
AAX69416/C
ID AAX69416 standard; RNA; 17 BP.
XX
XX AAX69416;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #711.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US17480.
XX
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX
XX (CHIR ) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 68; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

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CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.

XX SQ Sequence 17 BP; 3 A; 5 C; 1 G; 8 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 ATGGAAATATAAAGT 1601
 ||||| ||||| |||||
 DB 16 ATGGAAAGATAAAGT 1

RESULT 501
 AAT60201/c
 ID AAT60201 standard; DNA; 17 BP.

XX AC AAT60201;
 XX DT 03-FEB-1998 (first entry)
 XX DE Synthetic cdc2 kinase ribozyme recognition site #5.
 XX KW Ribozyme; hairpin; hammerhead; recognition site; cdc2 kinase;
 XX KW restenosis; growth factor; oncogene; vascular tissue;
 XX KW smooth muscle cell proliferation; ss.
 XX OS Synthetic.
 XX PN WO9710334-A2.
 XX PD 20-MAR-1997.
 XX PF 12-SEP-1996; 96WO-US14838.
 XX PR 12-SRP-1995; 95US-0527060.
 XX PA (IMMU-) IMMUSOL INC.
 XX PI Goldenberg T, Tritz R;
 XX WPI; 1997-202230/18.

XX PT New hairpin and hammerhead ribozyme(s) - which inhibit abnormal
 PT smooth muscle cell proliferation in vascular tissue, partic. for
 PT preventing or treating restenosis
 XX PS Example 1; Page 15; 50pp; English.

XX CC This sequence represents a ribozyme recognition site of the cdc2
 CC kinase gene which is cleaved by a hammerhead ribozyme at position 159.
 CC Novel hairpin and hammerhead ribozymes are being investigated for their
 CC ability to inhibit the activity of a growth factor (e.g. cdc2 kinase)
 CC responsible for abnormal smooth muscle cell (SMC) proliferation in
 CC vascular tissue leading to restenosis. The ribozymes can also directly
 CC block the production of oncogenes and cell regulatory factors involved
 CC with SMC growth following vascular injury.

XX SQ Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 TTATATAGATAAATT 1187
 ||||| ||||| |||||
 DB 16 TTATATAGATAAATT 1

RESULT 502

RAV96640
 ID AAV96640 standard; RNA; 17 BP.
 XX AC AAV96640;
 XX DT 01-MAR-1999 (first entry)
 XX DE Potato citrate synthase target sequence position 1334.
 XX KW Solanidine; glucosyltransferase; potato; citrate synthase; target;
 KW hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
 KW flower formation; cleavage; solanaceous plant; ss.
 XX OS Solanum tuberosum.
 XX PN WO9832843-A2.
 XX PD 30-JUL-1998.
 XX PF 14-JAN-1998; 98WO-US00738.
 XX PR 24-NOV-1997; 97US-0979416.
 XX PR 28-JAN-1997; 97US-0036545.
 XX PR 28-JAN-1997; 97US-0036599.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI McSwiggen JA, Zwick MG;
 XX WPI; 1998-427939/36.

XX PT New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid
 PT biosynthesis or regulating flowering
 XX PS Claim 53; Page 56; 79pp; English.

XX CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA-cleaving activity (e.g. ribozymes) which are capable of modulating
 CC the expression of plant genes: (i) involved in biosynthesis of
 CC alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334,
 CC and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase
 CC hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981,
 CC and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase
 CC target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195
 CC represent potato citrate synthase hammerhead and hairpin ribozymes,
 CC respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent
 CC potato citrate synthase target sequences. Ribozymes of the present
 CC invention can be used to inhibit the synthesis of toxic alkaloids in
 CC solanaceous plants, particularly potato but also tomato, pepper,
 CC aubergine and ditura or to inhibit flowering in potato, lettuce, spinach,
 CC cabbage, brussel sprouts, arugula, kale, collards, chard, beet, turnip,
 CC sweet potato and turf grass. Also the ribozymes can be used for RNA
 CC manipulation in the same way that restriction endonucleases are for DNA,
 CC as well as to examine genetic drift and mutations in plants and to
 CC detect specific RNA. The ribozymes can be targeted to specific genes or
 CC to consensus sequences within a family of related genes, and being
 CC catalytic need to be present at only very low concentrations.

XX SQ Sequence 17 BP; 5 A; 1 C; 4 G; 7 U; 0 other;

Query Match 1.0%; Score 12.9; DB 1; Length 17;
 Best Local Similarity 43.8%; Pred. NO. 4.3e+02;
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1283 TTATGTTTATCTGAA 1298
 ::::|::|::|::|
 DB 1 UUAAGUUUUAACUGAA 16

RESULT 503
 RAV95779
 ID AAV95779 standard; RNA; 17 BP.
 XX

PN W09821317-A1.
XX
PD 22-MAY-1998.
XX
PF 15-AUG-1997; 97WO-AU00520.
XX
PR 08-NOV-1996; 96AU-0003519.
XX
PA (WHEA-) WESTERN HEALTH CARE NETWORK.
XX
PI Aye TT, Bartholomew AI, De Man RA, Locarnini SA;
XX
DR WPI; 1998-297924/26.
XX
PT Variants of DNA virus replicating through RNA intermediate.
XX
PT especially hepatitis B - have mutations in genes for DNA polymerase,
XX
PT surface antigen or region of overlapping reading frames, and show
XX
PT reduced sensitivity to antiviral agents or antibodies
XX
PS Example 3; Page 19; 53pp; English.
XX
CC This sequence is a PCR primer for DNA encoding a fragment of a
CC Hepatitis B virus (HBV) DNA polymerase. The amplified fragment can be
CC mutated to give the variant of a DNA virus of the invention, that
CC replicates via an RNA intermediate. Detection of mutations in the
CC encoded protein sequence can be used in a method for determining if a HBV
CC isolate has reduced sensitivity to a nucleotide analogue or if its
CC surface antigen (sAg) has reduced interaction with antibodies. Mutations
CC in the DNA polymerase gene indicate (partial) resistance to nucleotide
CC analogues while those in the sAg gene indicate reduced interaction with
CC specific antibodies. Detecting sequences containing these mutations is
CC used to monitor anti-viral treatments (chemotherapy and/or vaccination)
CC and to screen for agents that can overcome the effects of such mutations
CC (potentially useful in long-term treatments with nucleotide analogues).
XX
SQ Sequence 17 BP; 5 A; 4 C; 1 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1556 CTCCTAAATTTTATTA 1571
DB 2 CTCCTAAATTTTATTA 17

RESULT 506
AAA18614/C
ID AAA18614 standard; RNA; 17 BP.
XX
AC AAA18614;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1840.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN W09950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US04507.

XX 27-MAR-1998; 98US-0079678.
XX (RIBO-) RIBOZYME PHARM INC.
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or
PT stability of an mRNA encoding an angiogenic factors -
XX
PS Claim 56; Page 106; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a tie-2 gene. AAA18615 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21501 to AAA21502 represent their corresponding target sequences;
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23263 to
CC AAA23264 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ Sequence 17 BP; 6 A; 3 C; 2 G; 6 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 975 TGTGAGACACTTTAA 990
DB 17 TTTGAGAGACTTTAA 2

RESULT 507
AAA18615/C
ID AAA18615 standard; RNA; 17 BP.
XX
AC AAA18615;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1841.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX

PN WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Payco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factor
 XX Claim 56; Page 106; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 XX and AAA19155 to AAA19222 represent their corresponding target sequences;
 XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 XX AAA21596 to AAA21688 represent their corresponding target sequences;
 XX AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 XX AAA23422 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 6 A; 3 C; 2 G; 6 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 975 TGTGGAAGCACTTTAA 990
 Db 16 TTGGAAGCACTTTAA 1
 RESULT 508
 ID AAA21157
 XX AAA21157 standard; RNA; 17 BP.
 XX AAA21157;
 XX 19-JUN-2000 (first entry)
 XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4383.
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;

KM tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factor
 XX Claim 55; Page 190; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 XX AAA21596 to AAA21688 represent their corresponding target sequences;
 XX AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 XX AAA23422 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 6 A; 2 C; 1 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 43.8%; Pred. No. 4.3e+02;
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 1002 ATACATAAAATATTT 1017
 Db 2 AUGCACTAAAUUUU 17
 RESULT 509
 AAA21200
 ID AAA21200 standard; RNA; 17 BP.
 XX AAA21200;
 XX 19-JUN-2000 (first entry)
 XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4426.
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW age related macular degeneration; cancer; diabetic retinopathy; arthritis;
 KW myopic degeneration; psoriasis; verruca vulgaris; neovascular glaucoma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 55; Page 193; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAL6775 to
 CC AAAL1767 and AAAL17561 to AAAL17622 represent ribozyme sequences for ARNT,
 CC and AAAL1768 to AAAL17560 and AAAL17623 to AAAL17684 represent their
 CC corresponding target sequences; AAAL17685 to AAAL18385 and AAAL19087 to
 CC AAAL19154 represent ribozyme sequences for Tie-2, and AAAL18386 to AAAL19086
 CC and AAAL19155 to AAAL19222 represent their corresponding target sequences;
 CC AAAL19223 to AAAL20361 and AAAL21501 to AAAL21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAAL20362 to AAAL21500 and
 CC AAAL21596 to AAAL21688 represent their corresponding target sequences;
 CC AAAL21689 to AAAL22475 and AAAL23263 to AAAL23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAAL22476 to AAAL23262, AAAL23343 to
 CC AAAL23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 3 A; 2 C; 4 G; 8 U; 0 other;
 SQ Sequence 17 BP; 3 A; 2 C; 4 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 17;
 Best Local Similarity 43.8%; Pred. No. 4.3e+02;
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 722 TTATTTTCAGGAAATG 737
 Db 2 UUUUUUUCAGGCAUUG 17
 RESULT 510
 ID AAA21469/c
 ID AAA21469 standard; RNA, 17 BP.
 XX AAA21469;
 XX 19-JUN-2000 (first entry)

XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4695.
 XX Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW age related macular degeneration; cancer; diabetic retinopathy; arthritis;
 KW myopic degeneration; psoriasis; verruca vulgaris; neovascular glaucoma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 55; Page 210; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAL6775 to
 CC AAAL1767 and AAAL17561 to AAAL17622 represent ribozyme sequences for ARNT,
 CC and AAAL1768 to AAAL17560 and AAAL17623 to AAAL17684 represent their
 CC corresponding target sequences; AAAL17685 to AAAL18385 and AAAL19087 to
 CC AAAL19154 represent ribozyme sequences for Tie-2, and AAAL18386 to AAAL19086
 CC and AAAL19155 to AAAL19222 represent their corresponding target sequences;
 CC AAAL19223 to AAAL20361 and AAAL21501 to AAAL21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAAL20362 to AAAL21500 and
 CC AAAL21596 to AAAL21688 represent their corresponding target sequences;
 CC AAAL21689 to AAAL22475 and AAAL23263 to AAAL23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAAL22476 to AAAL23262, AAAL23343 to
 CC AAAL23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 9 A; 0 C; 8 G; 8 U; 0 other;
 SQ Sequence 17 BP; 9 A; 0 C; 8 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1133 TTATAGTAAATTTATT 1148
 Db 15 TTATAAAATTTATT 1
 RESULT 511
 ID AAA21476/c

CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1045 TATTATGATTTATT 1060
 DB 17 TATTATTATTATTTT 2

RESULT 515
 ID AAZ24086/c
 XX AAZ24086 standard; DNA; 17 BP.

AC AAZ24086;

DT 04-FEB-2000 (first entry)

DE N. gonorrhoeae GC3 DNA fragment PCR primer 21.

XX GC3; species-specific detection; amplification; diagnosis; primer; ss.

OS Synthetic.

OS Neisseria gonorrhoeae.

XX DE19918479-A1.

XX 28-OCT-1999.

XX 23-APR-1999; 99DE-1018479.

XX 27-APR-1998; 98US-0067773.

XX (BECT) BECTON DICKINSON & CO.

XX You Q;

XX WPI; 1999-602549/52.

XX Isolated nucleic acid for the GC-3 fragment from Neisseria gonorrhoeae,
 PT useful for species-specific detection

XX Claim 3; Page 29; 37pp; German.

XX This invention describes a novel isolated nucleic acid (A) for the
 CC Neisseria gonorrhoeae GC-3 sequence. The isolated nucleic acid (A) and
 CC fragments of (A) are used for the species-specific detection of
 CC Neisseria gonorrhoeae in standard amplification or hybridization assays.
 CC Fragments of (A) are species-specific with no detectable cross-reaction
 CC with any other species, so they provide a rapid, reliable and selective
 CC (down to 10 genomic copies) diagnosis. AAZ24086-224090 represent PCR
 CC primers used in the identification of the N. gonorrhoeae GC3 fragment
 CC described in the method of the invention.

XX Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 756 TGATATTGAGCATC 771

DB 17 TGACATTGACCATC 2

RESULT 516
 ID AAX80243/c
 XX AAX80243 standard; DNA; 17 BP.

AC AAX80243;

DT 18-AUG-1999 (first entry)

DE Human BRCA1 wild type allele specific oligonucleotide SEQ ID NO:17.

XX Human; BRCA1; wild type; mutant; detection; primer; probe; cancer;
 KW breast cancer susceptibility gene; identification; variation;
 KW hybridisation; breast cancer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9929903-A2.

XX 17-JUN-1999.

XX 07-DEC-1998; 98WO-US25916.

XX 11-DEC-1997; 97US-0988706.

XX (GENE-) GENE LOGIC.

XX Allen AP, Angelly TS, Lawrence T, Lescallott JL;

PI Murphy PD, Olson SJ, Sadzewicz LK, Thurber DB, White MB;

PI Zeng B;

XX WPI; 1999-385623/32.

XX Mutants in BRCA gene associated with cancer

XX Claim 15; Page 64; 118pp; English.

XX The present invention describes fifteen new mutants of the breast cancer
 CC susceptibility gene BRCA1 gene, the mutations being located at
 CC nucleotides 421-2, 815, 926, 1506, 2034, 2428, 4643, 5053, 5210,
 CC 5396+40, 5150, 3904, 3888, 903, and 4164. AAX80235 to AAX80289 represent
 CC allele specific oligonucleotides for the mutant and wild type sequences
 CC of human BRCA1, and so are capable of identifying the normal or mutant
 CC gene by hybridisation. Methods from the present invention may be used
 CC for detecting a predisposition to cancer, especially breast cancer.

XX Sequence 17 BP; 6 A; 2 C; 3 G; 6 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 AATTTCGATTCAGTA 539

DB 17 AATTTCGATTCAGTA 2

RESULT 517

AXX80244/c

ID AAX80244 standard; DNA; 17 BP.

AC AAX80244;

DT 18-AUG-1999 (first entry)

DE Human BRCA1 mutant allele specific oligonucleotide SEQ ID NO:18.

XX Human; BRCA1; wild type; mutant; detection; primer; probe; cancer;

KW breast cancer susceptibility gene; identification; variation;

KW hybridisation; breast cancer; ss.

XX Synthetic.

OS Homo sapiens.

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XX PN WO9929903-A2.
XX XX
XX PD 17-JUN-1999.
XX XX
XX PF 07-DEC-1998; 98WO-US25916.
XX XX
XX PR 11-DEC-1997; 97US-0988706.
XX XX
XX PA (GENE-) GENE LOGIC.
XX XX
XX PI Allen AP, Angelly TS, Lawrence T, Lescallott JL;
XX PI Murphy PD, Olson SJ, Sadzewicz LX, Thurber DB, White MB;
XX PI Zeng B;
XX XX
XX DR WPI; 1999-385623/32.
XX XX
XX PT Mutants in BRCA gene associated with cancer
XX XX
XX PS Claim 16; Page 64; 118pp; English.
XX XX
XX CC The present invention describes fifteen new mutants of the breast cancer
XX CC susceptibility gene BRCA1 gene, the mutations being located at
XX CC nucleotides 421-2, 815, 926, 1506, 2034, 2428, 4643, 5053, 5210,
XX CC 5396+40, 5150, 3904, 3888, 903, and 4164. AAX80235 to AAX80289 represent
XX CC allele specific oligonucleotides for the mutant and wild type sequences
XX CC of human BRCA1, and so are capable of identifying the normal or mutant
XX CC gene by hybridisation. Methods from the present invention may be used
XX CC for detecting a predisposition to cancer, especially breast cancer.
XX XX
XX SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 AATTTCAGTTCAGTA 539
DB 17 AATTTCAGTTCAGTA 2

RESULT 518
AAV90992/C
ID AAV90992 standard; RNA; 17 BP.
AC AAV90992;
XX
XX DT 18-FEB-1999 (first entry)
XX
XX DE Human C-raf target site nucleotide position 513.
XX
XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX KW target; substrate; catalyst; modulation; expression; Raf gene;
XX KW delivery; screening; identification; synthesis; deprotection;
XX KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
XX KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9850530-A2.
XX XX
XX PD 12-NOV-1998.
XX XX
XX PF 05-MAY-1998; 98WO-US09249.
XX XX
XX PR 19-DEC-1997; 97US-0068212.
XX PR 09-MAY-1997; 97US-0046059.
XX PR 09-JUN-1997; 97US-0049002.
XX PR 03-JUL-1997; 97US-0051718.
XX PR 22-AUG-1997; 97US-0056808.
XX PR 02-OCT-1997; 97US-0061321.
XX PR 02-OCT-1997; 97US-0061324.
XX PR 05-NOV-1997; 97US-0064866.

(RIBO-) RIBOZYME PHARM INC.
Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
Karpeisky A, Kisich K, Matulic-Adamic J, McSwigen JA;
Parry I, Reynolds N, Sweedler D, Thompson J, Workman CT;
WPI; 1999-009494/01.

Identifying new catalytic nucleic acid that modulates selected
processes - especially ribozymes that cleave Raf RNA for treating
cancer, restenosis, and also new ribozymes and modified nucleoside
triphosphates used as antiviral agents and synthons

Claim 177; Page 147; 259pp; English.

A method has been developed for the identification of a nucleic acid
capable of modulating a process in a biological system. The method
comprises: (a) introducing into the system a random library of nucleic
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
a random sequence, and a catalytic domain (CD); and (b) identifying NAC
in systems where modulation has occurred and/or determining the sequence
of at least part of the SBDs in such systems. Nucleic acid molecules
with endonuclease activity and catalytic activity, from the present
invention, are used to modulate gene expression in plant and mammalian
cells and to cleave target nucleic acid, particularly for treating
systemic diseases caused by specific RNA, e.g. cancer, inflammation,
psoriasis, non-hepatic ascites and infection. They may also be used to
detect genetic drift and mutations in diseased cells and to determine
c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
expression of the Raf gene, are used to treat cancer, restenosis,
psoriasis or rheumatoid arthritis, or generally any condition associated
with the level of c-raf. Introduction of sugar/phosphate modifications
increases stability against nuclease and activity. AAV90922 to AAV93877
represent NACs that can be used in the method, specifically for
modulating the expression of a Raf gene.

Sequence 17 BP; 4 A; 4 C; 2 G; 7 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 446 AGCAATCTACTTCAA 461
DB 17 AGCAATCTACTTCAA 2

RESULT 519
AAV90993/C
ID AAV90993 standard; RNA; 17 BP.
XX
XX AC AAV90993;
XX
XX DT 18-FEB-1999 (first entry)
XX
XX DE Human C-raf target site nucleotide position 517.
XX
XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX KW target; substrate; catalyst; modulation; expression; Raf gene;
XX KW delivery; screening; identification; synthesis; deprotection;
XX KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
XX KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9850530-A2.
XX XX
XX PD 12-NOV-1998.
XX XX
XX PF 05-MAY-1998; 98WO-US09249.
XX XX
XX PR 19-DEC-1997; 97US-0068212.

```


CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the Tr2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX
 SQ Sequence 17 BP; 6 A; 0 C; 2 G; 9 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1144 TTATTATTATTAGAT 1159
 ||||| ||||| |||||
 DB 2 TTATTATTATTGAGAT 17

RESULT 522

AAFO3358
 ID AAF03358 standard; DNA; 17 BP.

AC AAF03358;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1653.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.

OS
 XX WO200061729-A2.

PN 19-OCT-2000.

XX 11-APR-2000; 2000WO-US09721.

XX 12-APR-1999; 99US-0129390.

PR (RIBO-) RIBOZYME PHARM INC.

PA Blatt L, Zwick M, Pavco P, McSwiggen J;

PI WPI; 2000-647423/62.

DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor

PT protein, interferon alpha and erythropoietin -

XX Claim 37; Page 93; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes

CC encoding the Tr2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement

CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in

CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.

XX Sequence 17 BP; 1 A; 4 C; 1 G; 11 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 985 CTTTACGTTTTCAT 1000
 ||||| ||||| |||||
 DB 1 CTTTCAGTTTTCCT 16

RESULT 523

AAFO4587

ID AAF04587 standard; DNA; 17 BP.

XX AAF04587;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #2103.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

XX WO200061729-A2.

PN 19-OCT-2000.

XX 11-APR-2000; 2000WO-US09721.

XX 12-APR-1999; 99US-0129390.

PR (RIBO-) RIBOZYME PHARM INC.

PA Blatt L, Zwick M, Pavco P, McSwiggen J;

PI WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor

PT protein, interferon alpha and erythropoietin -

XX Claim 4; Page 104; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes

CC encoding the Tr2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement

CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in

CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.

XX Sequence 17 BP; 10 A; 2 C; 2 G; 3 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1598 AAGTAAATATGAACA 1613
 ||||| ||||| |||||
 DB 1 AAATGAATATGAACA 16

RESULT 524

AAFO4941/c

ID AAF04941 standard; DNA; 17 BP.

XX AAF04941;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #2457.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

XX WO200061729-A2.

PN

XX

PD 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
XX WPI; 2000-647423/62.
DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 4; Page 111; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAATT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX Sequence 17 BP; 10 A; 2 C; 0 G; 5 T; 0 other;
SQ

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1143 TTTATTTTATTGTAGA 1158
DB 16 TTTATTTTATTGTAGA 1

RESULT 525
AAF05463
ID AAF05463 standard; DNA; 17 BP.
XX
XX AAF05463;
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #2682.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
XX WPI; 2000-647423/62.
DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 18; Page 117; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
XX Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
SQ

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1510 AAATACAGGCTTTAT 1525
DB 2 AAATACTAGTCTTTAT 17

RESULT 526
AAF05510
ID AAF05510 standard; DNA; 17 BP.
XX
XX AAF05510;
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #2729.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
XX WPI; 2000-647423/62.
DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 18; Page 118; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAATT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 other;
SQ

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 829 TGGATTTTCTCTT 844
DB 2 TGTATTTTCTCTGT 17

XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor,
XX PT interferon alpha; ss.
XX OS Homo sapiens.
XX FN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor,
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 18; Page 118; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
XX CC Protein (CDP). Inhibition of the repressors removes prevents
XX CC inhibition (and consequently increases expression of) genes involved in
XX CC the production of erythropoietin, granulocyte colony stimulating factor
XX CC protein and interferon alpha.
XX SQ Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 4.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 829 TGGATTTTTCCTGTT 844
XX Db 1 TGTATTTTTCCTGTT 16
XX
XX RESULT 528
XX AAF06334
XX ID AAF06334 standard; DNA; 17 BP.
XX AC AAF06334;
XX XX
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #3131.
XX XX
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX FN WO200061729-A2.
XX
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor,
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.

XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor,
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
XX CC Protein (CDP). Inhibition of the repressors removes prevents
XX CC inhibition (and consequently increases expression of) genes involved in
XX CC the production of erythropoietin, granulocyte colony stimulating factor
XX CC protein and interferon alpha.
XX SQ Sequence 17 BP; 7 A; 0 C; 1 G; 9 U; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 43.8%; Pred. No. 4.3e+02;
XX Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1616 TAAATATATATTTGTT 1631
XX Db 1 URAAAGAAUUGUUU 16
XX
XX RESULT 529
XX AAF06336/c
XX ID AAF06336 standard; DNA; 17 BP.
XX AC AAF06336;
XX XX
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #3133.
XX XX
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX FN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor,
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.

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XX CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRP-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX SQ Sequence 17 BP; 4 A; 1 C; 1 G; 11 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1248 AGATAAACACAAATA 1263
DB 17 AGATAAACACAAATA 2
||||| ||||| ||

RESULT 530
AAF06337/C
ID AAF06337 standard; DNA; 17 BP.
XX AC
XX AAF06337;
XX 16-FEB-2001 (first entry)
XX DT
XX Hammerhead ribozyme substrate #3134.
XX DE
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX KM
XX OS Homo sapiens.
XX XX
XX WO2000061729-A2.
XX FN
XX 19-OCT-2000.
XX FD
XX 11-APR-2000; 2000WO-US09721.
XX PF
XX 12-APR-1999; 99US-0129390.
XX PR
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX PI
XX WPI; 2000-647423/62.
XX DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.
XX CC
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRP-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX CC
XX Sequence 17 BP; 3 A; 1 C; 1 G; 12 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1248 AGATAAACACAAATA 1263
DB 17 AGATAAACACAAATA 1
||||| ||||| ||

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DB 16 AGATAAACACAAATA 1
RESULT 531
AAF06352
ID AAF06352 standard; DNA; 17 BP.
XX AC
XX AAF06352;
XX 16-FEB-2001 (first entry)
XX DT
XX Hammerhead ribozyme substrate #3149.
XX DE
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX KM
XX OS Homo sapiens.
XX XX
XX WO2000061729-A2.
XX FN
XX 19-OCT-2000.
XX PD
XX 11-APR-2000; 2000WO-US09721.
XX PF
XX 12-APR-1999; 99US-0129390.
XX PR
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX PI
XX WPI; 2000-647423/62.
XX DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 128; 164pp; English.
XX CC
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRP-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX CC
XX Sequence 17 BP; 6 A; 0 C; 1 G; 10 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TTTTAACTTTAAGAT 1542
DB 1 UUUUAAUUUUUAGAU 16
::: ||| ::|||:

RESULT 532
AA86571/C
ID AA86571 standard; DNA; 17 BP.
XX AC
XX AA86571;
XX 04-DEC-2000 (first entry)
XX DT
XX Cdc 2 kinase hammerhead ribozyme recognition site #2.
XX DE
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
XX KW restenosis; ss.
XX KM
XX OS Mammalia.
XX XX

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PN WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US28772.
XX
XX 04-DEC-1998; 98US-0110954.
XX
XX (IMM-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1
XX
XX Example 1; Page 17; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells.
XX The ribozyme is resistant to endonuclease activity and hence is
XX efficient in restenosis treatment.
XX
XX Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1172 TTTATAGATAAATTT 1187
XX ||||| |||||
XX DB 16 TTTATAGAGAAATTT 1
XX
XX RESULT 533
XX AAA25179
XX ID AAA25179 standard; DNA; 17 BP.
XX
XX AC AAA25179;
XX
XX DT 19-JUL-2000 (first entry)
XX
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1677.
XX
XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9954459-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 19-APR-1999; 99WO-US08547.
XX
XX PR 20-APR-1998; 98US-0082404.
XX
XX PR 23-JUN-1998; 98US-0103636.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX
XX DR WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target

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XX
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer
XX
XX Claim 77; Page 71; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA), in the same way that
XX restriction endonucleases are used with DNA. The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 other;
XX
XX Query Match 1.0%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1046 ATTTATGTTATTT 1061
XX ||||| |||||
XX DB 1 ATTTTGTTTTATTT 16
XX
XX RESULT 534
XX AAA25363
XX ID AAA25363 standard; DNA; 17 BP.
XX
XX AC AAA25363;
XX
XX DT 19-JUL-2000 (first entry)
XX
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1861.
XX
XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9954459-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 19-APR-1999; 99WO-US08547.
XX
XX PR 20-APR-1998; 98US-0082404.
XX
XX PR 23-JUN-1998; 98US-0103636.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX
XX DR WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target

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sequences, used to treat cancer -
Claim 77; Page 76; 148pp; English.
The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA). The combination of restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention.
Sequence 17 BP; 7 A; 0 C; 3 G; 7 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1538 AAGATGTTTATGTCG 1553
DB 2 AAAAGTTTATGTCG 17
RESULT 535
AAA25365
ID AAA25365 standard; DNA; 17 BP.
AC AAA25365;
XX 19-JUL-2000 (first entry)
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1863.
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX WO954459-A2.
XX 28-OCT-1999.
XX 19-APR-1999; 99WO-US08547.
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, McSwiggen JA, Karpetsky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer -
Claim 77; Page 76; 148pp; English.

Claim 77; Page 77; 148pp; English.
The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA). The combination of restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention.
Sequence 17 BP; 6 A; 1 C; 3 G; 7 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1539 AGATGTTTATGTCG 1554
DB 1 AAAAGTTTATGTCG 16
RESULT 536
AAA25366
ID AAA25366 standard; DNA; 17 BP.
AC AAA25366;
XX 19-JUL-2000 (first entry)
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1864.
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX WO954459-A2.
XX 28-OCT-1999.
XX 19-APR-1999; 99WO-US08547.
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, McSwiggen JA, Karpetsky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer -
Claim 77; Page 77; 148pp; English.

CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1541 ATGTTTATGTCGTC 1556
 DB 2 AAGTTTATGTCAC 17

RESULT 537
 AAA25453/C
 ID AAA25453 standard; DNA; 17 BP.

AC AAA25453;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

PN WO9954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99WO-US08547.

PR 20-APR-1998; 98US-0082404.

PR 23-JUN-1998; 98US-0103636.

PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;

DR WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -

PS Claim 77; Page 79; 148pp; English.

CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate

CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 TACAAAAACACACAAA 630

DB 17 TACAAAAACACACAAA 2

RESULT 538

AAA25454/C

ID AAA25454 standard; DNA; 17 BP.

AC AAA25454;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

PN WO9954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99WO-US08547.

PR 20-APR-1998; 98US-0082404.

PR 23-JUN-1998; 98US-0103636.

PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;

DR WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -

PS Claim 77; Page 79; 148pp; English.

CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen

CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.

XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 TACAAAAAACACAAA 630
 |||||
 DB 16 TACAAAAAACACAAA 1

RESULT 539
 AAA25487/c
 ID AAA25487 standard; DNA; 17 BP.

XX AC AAA25487;
 XX DT 19-JUL-2000 (first entry)
 XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1985.
 XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX FN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 19-APR-1999; 99WO-US08547.
 XX PR 20-APR-1998; 98US-0082404.
 XX PR 23-JUN-1998; 98US-0103636.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX DR WPI; 2000-013248/01.
 XX PT New nucleic acids that interact, and optionally cleave, target
 XX sequences, used to treat cancer -
 XX PS Claim 77; Page 80; 148pp; English.

XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting

CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.

XX SQ Sequence 17 BP; 4 A; 3 C; 1 G; 9 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1596 AAAAGTAAATATGAAA 1611
 |||||
 DB 16 AAAAGTAAATATGAAA 1

RESULT 540
 AAA25991/c
 ID AAA25991 standard; DNA; 17 BP.

XX AC AAA25991;
 XX DT 19-JUL-2000 (first entry)
 XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2489.
 XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX FN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 19-APR-1999; 99WO-US08547.
 XX PR 20-APR-1998; 98US-0082404.
 XX PR 23-JUN-1998; 98US-0103636.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX DR WPI; 2000-013248/01.
 XX PT New nucleic acids that interact, and optionally cleave, target
 XX sequences, used to treat cancer -
 XX PS Claim 77; Page 97; 148pp; English.

XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.

XX SQ Sequence 17 BP; 7 A; 1 C; 3 G; 6 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1055 TTTATTTAAGCATCAA 1070
DB 16 TTTATTTGACATCAA 1

RESULT 541
ABA77913/C
ID ABA77913 standard; DNA; 17 BP.
XX AC ABA77913;
XX DT 24-JAN-2002 (first entry)
XX DE BRCA1 mutation correcting oligonucleotide SEQ ID NO: 759.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MEH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antileptic; ss.

XX Homo sapiens.
XX WO200173002-A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-US09761.
XX PR 27-MAR-2000; 2000US-192176P.
XX PR 27-MAR-2000; 2000US-192179P.
XX PR 01-JUN-2000; 2000US-208538P.
XX PR 30-OCT-2000; 2000US-244989P.
XX PA (UYDE) UNIV DELAWARE.
XX PI Kniec EB, Gamper HB, Rice MC;
XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX Claim 7; Page 90; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic

CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MEH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention.

XX SQ Sequence 17 BP; 6 A; 2 C; 3 G; 6 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 524 AATTGCAATTTCAGTA 539
DB 16 AATTGCAATTTCAGTA 1

RESULT 542
ABA77914
ID ABA77914 standard; DNA; 17 BP.
XX AC ABA77914;
XX DT 24-JAN-2002 (first entry)
XX DE BRCA1 mutation correcting oligonucleotide SEQ ID NO: 760.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MEH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antileptic; ss.

XX Homo sapiens.
XX WO200173002-A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-US09761.
XX PR 27-MAR-2000; 2000US-192176P.
XX PR 27-MAR-2000; 2000US-192179P.
XX PR 01-JUN-2000; 2000US-208538P.
XX PR 30-OCT-2000; 2000US-244989P.
XX PA (UYDE) UNIV DELAWARE.
XX PI Kniec EB, Gamper HB, Rice MC;
XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX Claim 7; Page 90; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the

CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX Sequence 17 BP; 6 A; 3 C; 2 G; 5 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 AATTGCAATTTCAGTA 539

DB 2 AATTGCAATTTCAGTA 17

RESULT 543

ABA78613/c
 ID ABA78613 standard; DNA; 17 BP.

AC ABA78613;

XX 24-JAN-2002 (first entry)

DE APC mutation correcting oligonucleotide SEQ ID NO: 1459.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; Cancer; Factor V;
 XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 XX Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic;
 XX antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09761.

XX 27-MAR-2000; 2000US-192176P.

XX 27-MAR-2000; 2000US-192179P.

XX 01-JUN-2000; 2000US-208538P.

XX 30-OCT-2000; 2000US-244989P.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for

PT treating cystic fibrosis, comprises at least one mismatch and chemical

PT modification -

PS Claim 7; Page 133; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can

CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX Sequence 17 BP; 6 A; 4 C; 1 G; 6 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 4.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1577 TCTGATTGTATGAAA 1592

DB 16 TCTGTTTGTAAAGAAA 1

RESULT 544

ABA78614

ID ABA78614 standard; DNA; 17 BP.

XX ABA78614;

XX 24-JAN-2002 (first entry)

DE APC mutation correcting oligonucleotide SEQ ID NO: 1460.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; Cancer; Factor V;
 XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 XX Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic;
 XX antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09761.

XX 27-MAR-2000; 2000US-192176P.

XX 27-MAR-2000; 2000US-192179P.

XX 01-JUN-2000; 2000US-208538P.

XX 30-OCT-2000; 2000US-244989P.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for

PT treating cystic fibrosis, comprises at least one mismatch and chemical

PT modification -

PS Claim 7; Page 133; 294pp; English.

CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX Sequence 17 BP; 6 A; 1 C; 4 G; 6 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. NO. 4.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1577 TCTGATTGTATGGAA 1592

Db 2 TCTGTTTGAAGAA 17

RESULT 545

AAH61737/c

ID AAH61737 standard; DNA; 17 BP.

AC AAH61737;

DT 10-SEP-2001 (first entry)

DE Cdc 2 kinase hammerhead ribozyme recognition site SEQ ID NO:4161.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX recognition site; target; ribozyme binding site; eye disease; vulnery;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MIF;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiskilling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.

OS Homo sapiens.

OS Synthetic.

XX WO200130362-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29500.

XX 26-OCT-1999; 99US-0161532.

XX (IMMU-) IMMUSOL INC.

XX Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using

PT ribozymes that cleave RNA encoding cytokines involved in inflammation,

PT matrix metalloproteinases, growth factors and cell-cycle dependent

PT kinases -

XX Disclosure; Page 375; 408pp; English.

CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskilling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. NO. 4.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 TTTATTACATTAATTT 1187

Db 16 TTTAATGAGAAATTT 1

RESULT 546

AAF56150/c

ID AAF56150 standard; DNA; 17 BP.

XX AAF56150;

XX 17-APR-2001 (first entry)

XX Staphylococcus aureus agr regulatory region footprinted region B2.
 XX Staphylococcus aureus; SarA; staphylococcal accessory regulator A;
 XX agr; accessory gene regulator; antibacterial; SarA inhibitor;
 XX virulence gene; staphylococcal infection; DNA footprinting; ds.

OS Staphylococcus aureus.

XX WO200103686-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US18525.

XX 08-JUL-1999; 99US-0142793.

XX (UVAR-) UNIV ARKANSAS.

XX Huriburt BK, Smeltzer MS, Rechtin TM;

XX WPI; 2001-112567/12.

XX Identifying inhibitors of staphylococcal SarA (accessory regulator)
 XX which are useful for treating staphylococcal infections, comprises
 XX using specific binding sites of SarA protein on an accessory gene
 XX regulator locus -

XX Example; Fig 6B; 79pp; English.

XX The present sequence is given in a specification relating to a method for
 XX identifying inhibitors of SarA (staphylococcal accessory regulator)
 XX function involved in the expression of Staphylococcal virulence genes.
 XX The method comprises contacting a candidate inhibitor with a SarA
 XX binding site of the agr (accessory gene regulator) locus in solution

CC and assessing the binding of the candidate inhibitor to the Sara
CC binding site of the agr locus. The identified inhibitors are useful for
CC preventing and treating staphylococcal infections.

CC SQ Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1046 ATTATGTAATTTATT 1061
Db 17 AGTATGTAATTTATT 2

RESULT 547
ID ABK00430 standard; RNA; 17 BP.
AC ABK00430;
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX Human NOGO Hammerhead Ribozyme #430.
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04273.
XX
XX 11-FEB-2000; 2000US-181797P.
XX 28-FEB-2000; 2000US-185516P.
XX 06-MAR-2000; 2000US-187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWIRA B M.
XX
XX Blatt L, McSwiggen J, Chowira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukaemia,
XX and central nervous system injury -
XX
XX Claim 88; Page 72; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO).
XX The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN

CC motif) pr an amberszyme (cleaving RNA with an NGN triplet), a zinzyme
CC (cleaving RNA with a VGY motif). The CD20-targeting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOGO activity of the cell and
CC treat a patient having a condition associated with the level of NOGO. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NOGO-targeting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The
CC present sequence is a hammerhead ribozyme of the invention.

XX SQ Sequence 17 BP; 5 A; 2 C; 1 G; 9 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 909 CTCCTTTATTTCTAAG 924
Db 2 CUUAUUUUUUUAAG 17

RESULT 548
ID ABK00457 standard; RNA; 17 BP.
XX
XX AC ABK00457;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NOGO Hammerhead Ribozyme #457.
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04273.
XX
XX 11-FEB-2000; 2000US-181797P.
XX 28-FEB-2000; 2000US-185516P.
XX 06-MAR-2000; 2000US-187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWIRA B M.
XX
XX Blatt L, McSwiggen J, Chowira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukaemia,
XX and central nervous system injury -
XX
XX Claim 88; Page 72; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO).
XX The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN

XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX PI Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 XX Claim 88; Page 73; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is a hammerhead ribozyme of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 1 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e-02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1096 TAGAAGATGCAATCAATT 1111
 DB 17 TAGAAGATGCAATCAAT 2
 RESULT 549
 ABK01316/c
 ID ABK01316 standard; RNA; 17 BP.
 XX AC ABK01316;
 XX
 XX 12-MAR-2002 (first entry)
 DE Human NOGO Inozyme #586.
 XX Human; ss: antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04273.
 XX
 XX 11-FEB-2000; 2000US-181797P.
 XX 28-FEB-2000; 2000US-185516P.
 XX 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J.
 XX (CHOW/) CHOWRIRA B M.
 XX Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 XX and central nervous system injury -
 PS Claim 88; Page 87; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an inozyme of the invention.

SQ Sequence 17 BP; 5 A; 3 C; 1 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1096 TAGAAGATGAATCATT 1111
 DB 16 TAGAAGATGAATCAGT 1

RESULT 550
 ABK01612
 ID ABK01612 standard; RNA; 17 BP.
 AC ABK01612;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO G-Cleaver #68.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis (ALS);
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 FR 11-FEB-2000; 2000US-181797P.
 FR 28-FEB-2000; 2000US-185516P.
 FR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 93; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyze (cleaving RNA with an NKN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20-targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is a G-cleaver molecule of the invention.
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 4 G; 6 U; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. NO. 4.3e+02;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 429 ATGCCAGTGAACCTTC 444
 DB 1 AUGCAGUGAGGCUUC 16
 |||||
 |||||

RESULT 551
 ABK02193/c
 ID ABK02193 standard; RNA; 17 BP.
 XX
 AC ABK02193;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO DNazyme #105.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis (ALS);
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 FR 11-FEB-2000; 2000US-181797P.
 FR 28-FEB-2000; 2000US-185516P.
 FR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 93; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyze (cleaving RNA with an NKN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

(CHOW) CHOWRIRA B M.

Blatt L, McSwiggen J, Chowrira BM;
WPI; 2001-507195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury -

Claim 88; Page 114; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NIGO).

The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-targeting nucleic acid is used to cleave RNA of the NIGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NIGO activity of the cell and treat a patient having a condition associated with the level of NIGO. The treatment may further comprise the use of one or more therapies. In particular, the NIGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NIGO expression. The present sequence is a DNzyme molecule of the invention.

Sequence 17 BP; 9 A; 2 C; 3 G; 3 U; 0 other;

Query Watch 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1276 AAGTACATTATGTTT 1291
|||||
DB 16 AAGTCCATTGTTT 1

RESULT 552
ABV80683/C
ID ABV80683 standard; DNA; 17 BP.
AC ABV80683;
XX
DT 03-JAN-2003 (first entry)
DE Human HTPL scanning oligonucleotide SEQ ID 1929.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.

XX		
PN	EP1229046-A2.	
XX		
PD	07-AUG-2002.	
XX		
PF	28-JAN-2002; 2002EP-0001167.	
XX		
PR	30-JAN-2001; 2001WO-US000683.	
PR	30-JAN-2001; 2001WO-US000654.	
PR	30-JAN-2001; 2001WO-US000665.	
PR	30-JAN-2001; 2001WO-US000667.	
PR	30-JAN-2001; 2001WO-US000668.	
PR	30-JAN-2001; 2001WO-US000669.	
PR	23-MAY-2001; 2001US-0864761.	
PR	09-OCT-2001; 2001US-0327898.	
XX		
PA	(AEOM-) AEOMICA INC.	
XX		
PI	Zhan J;	
DR	WPI; 2002-676582/73.	
XX		
PT	Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -	
XX		
PS	Example 2; Page 316; 718pp; English.	
XX		
CC	The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (\$ for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.	
XX		
SQ	Sequence 17 BP; 5 A; 3 C; 2 G; 7 T; 0 other;	
	Query Match 1.0%; Score 12.8; DB 1; Length 17;	
	Best Local Similarity 87.5%; Pred. No. 4.3e+02;	
	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1457 GTTATATAGTCACAA 1472 17 GCATTATGATACAAA 2	
Db		
	RESULT 553	
	ABV80685/c	
ID	ABV80685 standard; DNA; 17 BP.	
XX		
AC	ABV80685;	
XX		
DT	03-JAN-2003 (first entry)	
XX		
DE	Human HTPL scanning oligonucleotide SEQ ID 1931.	
XX		
KW	Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;	
KW	human testis expressed Patched like protein; testis; adrenal; liver;	
KW	male germ cell development; bone marrow; brain; kidney; lung; placenta;	
KW	prostate; skeletal muscle; colon; male infertility; cancer;ss.	

KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX OS
XX Homo sapiens.
XX EP1229046-A2.
XX PD 07-AUG-2002.
XX PF 28-JAN-2002; 2002EP-0001167.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 23-MAY-2001; 2001US-0864761.
XX PR 09-OCT-2001; 2001US-0327898.
XX (AEOM-) AEOMICA INC.
XX PA
XX Zhan J;
XX WP1; 2002-676582/73.
XX DR
XX Novel isolated human testis expressed Patched like protein (HTPL),
XX useful for identifying agonist and antagonist and specific binding
XX partners, and for treating subjects having defects in HTPL -
XX
XX Example 2; Page 630; 718pp; English.
XX PS
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention.
XX SQ Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 603 TTTATTTGAATCTACA 618
DB 1 TTTATTTGAATCTACA 16
RESULT 556
ABV90149/c
ID ABV90149 standard; DNA; 17 BP.
XX AC ABV90149;
XX XX
XX 23-DEC-2002 (first entry)
XX

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 862.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS
XX Homo sapiens.
XX EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-0001165.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 30-JAN-2001; 2001WO-US00670.
XX PR 23-MAY-2001; 2001US-0864761.
XX PR 10-OCT-2001; 2001US-0328205.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WP1; 2002-684061/74.
XX DR
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
XX POSHL-1, useful for treating disorders associated with decreased
XX expression or activity of human POSHL1 -
XX
XX Example 2; SEQ ID NO 862; 60pp + Sequence Listing; English.
XX PS
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating
XX caused by altered expression of human POSHL1 including diagnosing and
XX treating cancer, they are useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention.
XX Note: The present sequence did not form part of the printed
XX specification, but is based on sequence information supplied to Derwent
XX by the European Patent Office.
XX SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1335 CAGCTCTGTCATTCGCC 1350
DB 17 CAGCTCTGTCATTCGCC 2
RESULT 557
ABV90150/c
ID ABV90150 standard; DNA; 17 BP.
XX

AC ABV90150;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 863.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-0001165.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 30-JAN-2001; 2001WO-US00670.
XX 23-MAY-2001; 2001US-0844761.
XX 10-OCT-2001; 2001US-0328205.
XX (ABOM-) ABOMICA INC.
XX Shannon M;
XX WPI; 2002-684063/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX
XX Example 2; SEQ ID NO 863; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB83999), a sequence having 65% sequence identity to (SI1),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;
SQ
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. NO. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1335 CAGCTCTGCTCATGCC 1350
DB 16 CACTCTGCTCTGCTGCC 1

RESULT 558
ABK56195
ID ABK56195 standard; RNA; 17 BP.
XX
XX AC ABK56195;
XX
XX 02-JUL-2002 (first entry)
XX Human CLCA1 gene enzymatic nucleic acid #566.
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
XX Homo sapiens.
XX WO200211674-A2.
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US24970.
XX 09-AUG-2000; 2000US-224383P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (SYNT) SYNTX USA LLC.
XX (THOM/) THOMPSON J.
XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX Grupe A;
XX WPI; 2002-217145/27.
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX
XX Claim 4; Page 63; 152pp; English.
XX
XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.
XX
XX Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;
SQ
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
Qy 1133 TTATAGTAAATTTATT 1148
DB 2 UUAUACUAAAGUAAU 17
RESULT 559
ABK56693/c
ID ABK56693 standard; RNA; 17 BP.

XX AC ABK56693;
XX DT 02-JUL-2002 (first entry)
XX DE Human CLCA1 gene enzymatic nucleic acid #1064.
XX KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX KW acetylcysteine.
XX OS Homo sapiens.
XX PN WO200211674-A2.
XX PD 14-FEB-2002.
XX PP 09-AUG-2001; 2001WO-US24970.
XX PR 09-AUG-2000; 2000US-224383P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (SYNT) SYNTX USA LLC.
XX PA (THOM/) THOMPSON J.
XX PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX PI Grupe A;
XX DR WPI; 2002-217145/27.
XX DT Enzymatic polynucleotide that down regulates expression of chloride
XX PT channel calcium activated gene, useful for treating Chronic obstructive
XX PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX PS Claim 4; Page 78; 152pp; English.
XX CC The invention relates to enzymatic nucleic acid molecules that down
XX CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX CC by cleaving RNA derived from the genes. The nucleic acid sequences are
XX CC useful as pharmaceutical agents for treating conditions such as chronic
XX CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX CC that are related to or will respond to the levels of CLCA1 in a cell or
XX CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX CC hence, are useful for treatment of a patient having a condition
XX CC associated with the level of CLCA1, where the invention further comprises
XX CC the use of one or more therapies under conditions suitable for the
XX CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX CC nucleic acids of the invention are also used as diagnostic tools to
XX CC examine genetic drift and mutations within diseased cells or to detect
XX CC the presence of CLCA1 RNA in a cell. This sequence represents an
XX CC enzymatic nucleic acid molecule of the invention.
XX SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 722 TTAATTTCAGGAATTG 737
DB 17 TTAATTTCAGGCTCTG 2
RESULT 560
ABK56852
ID ABK56852 standard; RNA; 17 BP.
XX AC ABK56852;
XX DT 02-JUL-2002 (first entry)
XX DE Human CLCA1 gene enzymatic nucleic acid #1064.

DT 02-JUL-2002 (first entry)
XX Human CLCA1 gene enzymatic nucleic acid #1223.
DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX KW acetylcysteine.
XX OS Homo sapiens.
XX PN WO200211674-A2.
XX PD 14-FEB-2002.
XX PP 09-AUG-2001; 2001WO-US24970.
XX PR 09-AUG-2000; 2000US-224383P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (SYNT) SYNTX USA LLC.
XX PA (THOM/) THOMPSON J.
XX PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX PI Grupe A;
XX DR WPI; 2002-217145/27.
XX DT Enzymatic polynucleotide that down regulates expression of chloride
XX PT channel calcium activated gene, useful for treating Chronic obstructive
XX PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX PS Claim 4; Page 84; 152pp; English.
XX CC The invention relates to enzymatic nucleic acid molecules that down
XX CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX CC by cleaving RNA derived from the genes. The nucleic acid sequences are
XX CC useful as pharmaceutical agents for treating conditions such as chronic
XX CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX CC that are related to or will respond to the levels of CLCA1 in a cell or
XX CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX CC hence, are useful for treatment of a patient having a condition
XX CC associated with the level of CLCA1, where the invention further comprises
XX CC the use of one or more therapies under conditions suitable for the
XX CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX CC nucleic acids of the invention are also used as diagnostic tools to
XX CC examine genetic drift and mutations within diseased cells or to detect
XX CC the presence of CLCA1 RNA in a cell. This sequence represents an
XX CC enzymatic nucleic acid molecule of the invention.
XX SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 U; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 4.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1245 TTCAGATTAACACAA 1260
DB 2 UUCAGCUGAACACAA 17
RESULT 561
ABK56963/C
ID ABK56963 standard; RNA; 17 BP.
XX AC ABK56963;
XX DT 02-JUL-2002 (first entry)
XX DE Human CLCA1 gene enzymatic nucleic acid #1334.

XX Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX acetylcysteine.
OS Homo sapiens.
XX W0200211674-A2.
XX 14-FEB-2002.
XX 09-AUG-2001; 2001WO-US24970.
XX 09-AUG-2000; 2000US-224383P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
PI WPI; 2002-217145/27.
XX Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating Chronic obstructive
pulmonary disease (COPD), chronic bronchitis and asthma -
XX Claim 4; Page 87; 152pp; English.
XX The invention relates to enzymatic nucleic acid molecules that down
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
by cleaving RNA derived from the genes. The nucleic acid sequences are
useful as pharmaceutical agents for treating conditions such as chronic
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
fibrosis, obstructive bowel syndrome and any other diseases or conditions
that are related to or will respond to the levels of CLCA1 in a cell or
tissue. The sequences are useful for reducing CLCA1 activity in a cell or
tissue. The sequences are useful for a patient having a condition
associated with the level of CLCA1, where the invention further comprises
the use of one or more therapies under conditions suitable for the
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
nucleic acids of the invention are also used as diagnostic tools to
examine genetic drift and mutations within diseased cells or to detect
the presence of CLCA1 RNA in a cell. This sequence represents an
enzymatic nucleic acid molecule of the invention.
XX Sequence 17 BP; 8 A; 3 C; 2 G; 4 U; 0 other;
SQ Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 722 TTAATTCAGGCTCTG 737
DB 16 TTAATTCAGGCTCTG 1
RESULT 562
ABK57058
ID ABK57058 standard; RNA; 17 BP.
AC ABK57058;
XX 02-JUL-2002 (first entry)
XX Human CLCA1 gene enzymatic nucleic acid #1429.
DE Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX acetylcysteine.
OS Homo sapiens.
XX W0200211674-A2.
XX 14-FEB-2002.
XX 09-AUG-2001; 2001WO-US24970.
XX 09-AUG-2000; 2000US-224383P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
PI WPI; 2002-217145/27.
XX Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating Chronic obstructive
pulmonary disease (COPD), chronic bronchitis and asthma -
XX Claim 4; Page 90; 152pp; English.
XX The invention relates to enzymatic nucleic acid molecules that down
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
by cleaving RNA derived from the genes. The nucleic acid sequences are
useful as pharmaceutical agents for treating conditions such as chronic
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
fibrosis, obstructive bowel syndrome and any other diseases or conditions
that are related to or will respond to the levels of CLCA1 in a cell or
tissue. The sequences are useful for reducing CLCA1 activity in a cell,
hence, are useful for treatment of a patient having a condition
associated with the level of CLCA1, where the invention further comprises
the use of one or more therapies under conditions suitable for the
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
nucleic acids of the invention are also used as diagnostic tools to
examine genetic drift and mutations within diseased cells or to detect
the presence of CLCA1 RNA in a cell. This sequence represents an
enzymatic nucleic acid molecule of the invention.
XX Sequence 17 BP; 6 A; 1 C; 2 G; 8 U; 0 other;
SQ Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 1136 TAGTAAATTTATTTTA 1151
DB 1 UACUAAAGUAGUUUA 16
RESULT 563
ABK18668/C
ID ABK18668 standard; RNA; 17 BP.
AC ABK18668;
XX 09-APR-2002 (first entry)
XX Human ERG G-cleaver ribozyme target sequence Seq ID No 1315.
DE Human, hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 OS Homo sapiens.
 XX WO200188124-A2.
 XX 22-NOV-2001.
 XX 16-MAY-2001; 2001WO-US15866.
 XX 16-MAY-2000; 2000US-0572021.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX Claim 4; Page 84; 149pp; English.
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX Sequence 17 BP; 7 A; 1 C; 2 G; 7 U; 0 other;
 SQ
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1235 AAATTTTCATTTCAGA 1250
 DB 16 AAATTTTCATTTCAGA 1
 RESULT 564
 ID ABK18697/c
 XX ABK18697 standard; RNA; 17 BP.
 AC ABK18697;
 XX
 DT 09-APR-2002 (first entry)

XX Human ERG G-cleaver ribozyme target sequence Seq ID No 1344.
 DE
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnarary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX Homo sapiens.
 OS
 XX WO200188124-A2.
 XX 22-NOV-2001.
 XX 16-MAY-2001; 2001WO-US15866.
 XX 16-MAY-2000; 2000US-0572021.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX Claim 4; Page 85; 149pp; English.
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX Sequence 17 BP; 9 A; 0 C; 3 G; 5 U; 0 other;
 SQ
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1171 TTTTATTAGATATATT 1186
 DB 17 TTTTATTATACATATT 2

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RESULT 565
ABT34683/c
ID ABT34683 standard; DNA; 17 BP.
XX AC
XX AC ABT34683;
XX DT
XX DT 12-JUN-2003 (first entry)
XX DE
XX DE Tumour suppression related human fukutin oligo SEQ ID No 320.
XX KW
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2003025175-A2.
XX PD
XX PD 27-MAR-2003.
XX PF
XX PF 17-SEP-2002; 2002WO-IB04208.
XX PR
XX PR 17-SEP-2001; 2001FR-0011978.
XX PA
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX PI Telerman A, Amson R, Tuijnder M;
XX DR
XX DR WPI; 2003-313353/30.
XX PT
XX PT New isolated nucleic acid, useful for treating viral diseases
XX PT associated with tumors and cell degeneration, also related
XX PT polypeptides, antibodies and transfected cells
XX PS
XX PS Disclosure; Page 71; 720pp; French.
XX CC
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15
XX CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
XX CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
XX CC sequence that hybridizes to them under highly stringent conditions, or
XX CC the complement of any of them, or the corresponding RNA. The novel
XX CC isolated nucleic acids of the invention are useful as probes and primers
XX CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
XX CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
XX CC and for production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention.
XX SQ
XX Sequence 17 BP; 2 A; 2 C; 5 G; 8 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 438 AAACCTCAAGCAATC 453
DB 16 AAACCTCAAGCAATC 1
RESULT 566
ABT34698/c
ID ABT34698 standard; DNA; 17 BP.
XX AC
XX AC ABT34698;
XX DT
XX DT 12-JUN-2003 (first entry)
XX DE
XX DE Tumour suppression related human fukutin oligo SEQ ID No 335.
XX KW
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2003025175-A2.
XX PD
XX PD 27-MAR-2003.
XX PF
XX PF 17-SEP-2002; 2002WO-IB04208.
XX PR
XX PR 17-SEP-2001; 2001FR-0011978.
XX PA
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX PI Telerman A, Amson R, Tuijnder M;
XX DR
XX DR WPI; 2003-313353/30.
XX PT
XX PT New isolated nucleic acid, useful for treating viral diseases
XX PT associated with tumors and cell degeneration, also related
XX PT polypeptides, antibodies and transfected cells
XX PS
XX PS Disclosure; Page 73; 720pp; French.
XX CC
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15
XX CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
XX CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
XX CC sequence that hybridizes to them under highly stringent conditions, or
XX CC the complement of any of them, or the corresponding RNA. The novel
XX CC isolated nucleic acids of the invention are useful as probes and primers
XX CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
XX CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
XX CC and for production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention.
XX SQ
XX Sequence 17 BP; 5 A; 1 C; 3 G; 8 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1462 TTATGTACAAATAGAT 1477
DB 17 TAATCTACAAATAGAT 2
RESULT 567
ABT35053/c
ID ABT35053 standard; DNA; 17 BP.

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